

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 17, 2004, 16:54:34 ; Search time 4445 Seconds  
(without alignments)

2905.787 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543

Sequence: 1 MTEQAISFAKDFLAGGIAAA.....LRNGGAFVLVLYDELKKVI 298

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Fgapop 6.0 , Fgapext 7.0  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	1543	100.0	897	6	AX134720	AX134720 Sequence
4	1543	100.0	897	6	AX301848	AX301848 Sequence
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25	1446	93.7	1266	5	AF506216	AF506216 Danio rer
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27	1446	93.7	1297	5	AY398420	AY398420 Danio rer
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# ALIGNMENTS

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LOCUS
DEFINITION Production of adenine nucleotide translocator (ANT), novel ANT
ligand, and screening assay thereof.
ACCESSION
VERSION BD249697.1 GI:33059467
KEYWORDS JP 2002539761-A/3.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 897)
AUTHORS Anderson,C.M., Davis,R.E., Clevenger,W., Wiley,S.E., Miller,S.W.,
Szabo,R.R. and Ghosh,S.S.
TITLE Production of adenine nucleotide translocator (ANT), novel ANT
ligand, and screening assay thereof
JOURNAL Patent: JP 2002539761-A 3 26-NOV-2002;
MITOKOR
COMMENT OS Homo sapiens (human)
PN JP 2002539761-A/3
PD 26-NOV-2002
PR 03-NOV-1999 JP 2000579742
PF 03-NOV-1998 US 09/185904,08-SEP-1999 US 09/393441 PI
CHRISTEN M ANDERSON,ROBERT E DAVIS,WILLIAM CLEVENGER,SANDRA PI
EILEEN WILEY.
PI SCOTT W MILLER,TOMAS R SZABO,SOURMITRA S GHOSH PC
C12N15/09,A61K31/704,A61K31/7056,A61K31/7064, PC
A61K45/00,
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A61P25/18,
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PC C07K1/22,
PC C07K14/47,C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10 PC
C12P21/02,C12Q1/02,
PC G01N33/15,G01N33/50,C12N15/00,C12N5/00
CC Production of adenine nucleotide translocator (ANT), novel ANT
ligand, and
CC screening assay thereof
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Pred. No.: 1,03e-144 Length: 897
Score: 1543.00 Matches: 298
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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LOCUS
DEFINITION Sequence 3 from patent US 6562563..
ACCESSION AR316657
VERSION AR316657.1 GI:33695603
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 897)
MURPHY,A.N., CLEVENGER,W., WILEY,S.E., ANDREYEV,A.Y., FRIGERI,L.G.,
VELECELEBI,G. and DAVIS,R.E.
TITLE Compositions and methods for determining interactions of
mitochondrial components, and for identifying agents that alter
such interactions
JOURNAL Patent: US 6562563-A 3 13-MAY-2003;
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1..897
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Pred. No.: 1,03e-144 Length: 897
Score: 1543.00 Matches: 298
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LOCUS  
DEFINITION  
Sequence 3 from Patent WO0132876.  
ACCESSION  
AX134720  
VERSION  
AX134720.1 GI:14271237  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Murphy, A.N., Clevenger, W., Wiley, S.E., Andreyev, A.Y., Frigeri, L.G.,  
Velicelabi, G. and Davis, R.E.  
TITLE Compositions and methods for determining interactions of  
mitochondrial components, and for identifying agents that alter  
such interactions  
JOURNAL Patent: WO 0132876-A 3 10-MAY-2001;  
MITOKOR (US)

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Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-09-811-094-33 (1-298) x AX134720 (1-897)

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DB 841 GGCATGGGGGGCGCTTCTGCTGCTCTGTACGACGAGCTCAAGAGAGTGCATC 894

QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 DB 661 ACAGCGGCGCGCGGTGTCTCTCCCTTCACACGCGTGGCGCGGCATGATG 720  
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260  
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RESULT 4  
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 DEFINITION Sequence 3 from Patent WO0185944.  
 ACCESSION AX301848  
 VERSION AX301848.1 GI:17382905  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Anderson, C.M., Davis, R.E., Clevenger, W., Wiley, S.E., Miller, S.W., Szabo, T.R., Ghosh, S.S., Mocs, W.H., Pei, Y., and Carroll, A.K.  
 TITLE Production of adenine nucleotide translocator (ant), novel ant  
 JOURNAL ligands and screening assays therefor  
 PATENT: WO 0185944-A 3 15-NOV-2001;  
 MITOKOR (US)

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 Best Local Similarity: 100.00% Indels: 0  
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 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
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 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
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 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 DB 661 ACAGCGGTGGCGGCGGTGTCTTACCCCTTCACACGCGTGGCGGCGCATGATGATG 720  
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260  
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RESULT 5  
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 DEFINITION Homo sapiens soluble carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, mRNA (cDNA clone MGC:2387 IMAGE:2824067), complete cds.  
 ACCESSION BC008935  
 VERSION BC008935.2 GI:33874058  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1184)  
 AUTHORS Klausner, R.D., Collins, P.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Alschul, S.P., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y., Krzywinski, M.I., Skalska, U., Smalios, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Warra, M.A.  
 TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)





JOURNAL Patent: US 659662-A 687 27-MAY-2003;

## FEATURES

source

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/mol\_type="genomic DNA"

## ORIGIN

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US-09-811-094-33 (1-298) x AR339196 (1-1212)

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QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheIysAspIysTyrIysGlnIlePheLeu 100  
DB 371 TACTTCCCACTCAAGCCCTCACTTCGCTTCAAGGATAGTACAGCAGATCTTCTCTG 430  
QY 101 GlyGlyValAspIysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
DB 431 GGGGGCGTGGAACAGACAGCAGTCTTGAGGTACTTTCGGGCAACCTTGGCGCTCCGGC 490  
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValIysProLeuAspPheAlaArgThrArg 140  
DB 491 GGTGCGCGCGCGACCTCCCTCTGCTGTGTACCGCTGGATTCGCCAGACCCCGC 550  
QY 141 LeuAlaAlaAspValGlyIysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
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DB 611 CTGGTGAGATCACCAAGTCCGAGGATCCGGGCTGTACCAAGGCTTCAGTGTCTCC 670  
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DB 671 GTGCAGGCGCATCATCTACCGCGCGCTACTTCGCGCTGTACGATACGCGCAAGGCG 730  
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QY

DB

RESULT 7

BC007295

LOCUS

DEFINITION

Homo sapiens solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, mRNA (cDNA clone MGC:15671 IMAGE:3349670), complete cds.

ACCESSION

BC007295

VERSION

BC007295.1

KEYWORDS

MGC.

SOURCE

Homo sapiens

ORGANISM

REFERENCE

AUTHORS

1. (bases 1 to 1308)

Strausberg,R.D., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Haieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshnyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Sanchez,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Fahey,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Kzywinski,M.I., Skalska,U., Smalhus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2. (bases 1 to 1308)

Strausberg,R.

Direct Submission

Submitted (01-MAY-2001)

National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK

NIH-MGC Project URL: http://mgc.nci.nih.gov

Contact: MGC help desk

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Varon Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candace McLeavy, Steven

Nees, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacques

Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Scott,

Michael Thorne, Mitranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov

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Location/Qualifiers

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US-09-811-094-33 (1-298) x BC007295 (1-1308)

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VERSION AY007135.1 GI:9956038
KEYWORDS FLI_CDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLES Andersson B., Wentland M.A., Ricafrente J.Y., Liu W. and Gibbs R.A.
JOURNAL A 'double adaptor' method for improved shotgun library construction
MEDLINE Anal. Biochem. 236 (1), 107-113 (1996)
PUBMED 96207227
PUBMED 8619474
REFERENCE 2 (bases 1 to 1344)
AUTHORS Yu, W., Andersson B., Worley, K.C., Muzny D.M., Ding, Y., Liu, W.,
Ricafrente, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.
TITLES Large-scale concatenation cDNA sequencing
JOURNAL Genome Res. 7 (4), 353-358 (1997)
MEDLINE 97264341
PUBMED 9110174
REFERENCE 3 (bases 1 to 1344)
AUTHORS Zhou, J., Yu, W., Tang, H., Mei, G., Tsang, Y.T.M., Bouck, J., Gibbs, R.A.
and Margolin, J.F.
TITLES Direct Submission
JOURNAL Submitted (24-JUL-2000) Human Genome Sequencing Center and Texas
Children's Cancer Center, Baylor College of Medicine, Houston, TX
77030, USA
COMMENT The clone request should be directed to Dr. J. Margolin at
Pediatrics-Hematology & Oncology, Texas Children's FEIGIN Center
102514, Houston, Texas 77030, USA. Telephone: 713-770-4583
margolin@bcm.tmc.edu.
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Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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US-09-811-094-33 (1-298) x BC007850 (1-1357)

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DEFINITION Homo sapiens soluble carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, mRNA (cDNA clone MGC:29984 IMAGE:5141625), complete cds.

ACCESSION BC031912  
VERSION BC031912.1 GI:21594692  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1399)  
AUTHORS Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalley S., Schnerk A., Schein J.E., Jones S.J. and Marra M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
MEDLINE 22398257



Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1457)  
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, P., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, W.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raja, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wozley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerbach, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)  
 22388257  
 12477932

2 (bases 1 to 1457)  
 Strausberg, R.

Direct Submission  
 Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:14250566.  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)  
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
 Gaithersburg, Maryland;  
 Contact: [nisc.mgc@nhgri.nih.gov](mailto:nisc.mgc@nhgri.nih.gov)  
 Web site: <http://www.nisc.nih.gov/>

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, P.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgoun, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <http://image.llnl.gov>  
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RESULT 12  
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 ACCESSION BC014775  
 VERSION BC014775.1 GI:15928607  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1455)  
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapkota, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smalusi, D.E., Schnerch, A., Schein, J.E., Jones, S.G., and Marra, M.A., M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 TITLE Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 JOURNAL 2338257  
 MEDLINE 1247932  
 PUBMED 2 (bases 1 to 1455)  
 REFERENCE Strausberg, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louissege, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at: <http://image.llnl.gov>  
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VERSION     AB088686.1  GI:22775581
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SOURCE      Gallus gallus (chicken)
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            Phasianinae; Gallus.
REFERENCE   1
            Toyomizu, M., Ueda, M., Sato, S., Seki, Y., Sato, K. and Akiba, Y.
            Cold-induced mitochondrial uncoupling and expression of chicken UCP
            and ANT mRNA in chicken skeletal muscle
            FEBS Lett. (2002) in press
            Direct Submission
            Ueda, M., Seki, Y., Sato, S., Akiba, Y. and Toyomizu, M.
            Submitted (24-JUL-2002) Masaaki Toyomizu, Tohoku University, Life
            Science, Graduate School of Agriculture, 1-1
            Tsutsumidori-Amamiyamachi, Sendai, Miyagi 981-8555, Japan
            (E-mail: toyomizu@bios.tohoku.ac.jp,
            URL: http://www.bios.tohoku.ac.jp/animutr/, Tel: 81-22-717-8690,
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US-09-811-094-33 (1-298) x AB088686 (1-1010)

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ACCESSION   BC056160
VERSION     BC056160.1  GI:33525217
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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
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            Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

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Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, X.S., Krzyzanski, M.I., Skalska, J., Smallos, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

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12477932  
2 (bases 1 to 1251)  
Strausberg, R.  
Direct Submission  
Submitted (04-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
BC Cancer Agency, Vancouver, BC, Canada  
[info@bcgsc.bc.ca](mailto:info@bcgsc.bc.ca)  
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Brin Garland, Ran Guin, Leticia Hsiao, Martin Krzyzanski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Jiisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smallos, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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**TITLE**  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

**REMARK**  
COMMENT

ORIGIN  
Alignment Scores:  
Pred. No.: 1251  
Score: 1463.00  
Percent Similarity: 97.30%  
Best Local Similarity: 92.91%  
Query Match: 94.82%  
Indels: 0  
Gaps: 9  
US-09-811-094-33 (1-298) x BC056160 (1-1251)

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Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
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**FEATURES**  
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gene  
CDS  
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Wed Aug 18 16:42:48 2004

us-09-811-094-33.rge

Page 16

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Job time : 4461 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 17, 2004, 16:56:19 ; Search time 473 Seconds  
(without alignments)  
2676.455 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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6	1543	100.0	2035	4	AAI60583 Human pol
7	1510	97.9	2592	7	ABX63152 Human cdn
8	1463	94.8	1225	6	AAI46635 Human ins

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11	1454	94.2	897	6	AAS16689	DNA encod
12	1424	92.3	1196	6	ABK63420	Rat seque
13	1424	92.3	1196	9	ADB57820	Toxicity-
14	1424	92.3	1196	9	ADB52341	Primary r
15	1418	91.9	2213	7	ACC46652	Human dit
16	1417	91.8	1156	5	AAS91243	DNA encod
17	1412	91.5	1177	2	AAV36479	Ant1 CDNA
18	1405	91.1	1259	2	AAV36480	Ant1 CDNA
19	1385	89.8	894	3	AAD00519	Human ade
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22	1385	89.8	1024	7	ABZ83302	Toxicolog
23	1385	89.8	1320	6	ABSE5029	Invertebr
24	1356	87.9	1116	6	ABL169347	Prostate
25	1356	87.9	1116	6	ABK83761	Human cdn
26	1356	87.9	1116	6	ABN95598	Gene #209
27	1289	83.5	552	9	ADC39187	Novel hum
28	1276	82.7	936	9	ADC39191	Novel hum
29	1254	81.3	1581	4	ABL18531	Drosophil
30	1254	81.3	1750	4	ABL20967	Drosophil
31	1247	80.8	905	9	ADC39082	Novel hum
32	1193	77.3	2706	4	AAS29836	Human cvt
33	1193	77.3	2706	4	AAS35083	DNA #33 e
34	1193	77.3	2706	9	ADC46525	Human neo
35	1184	76.8	925	6	ABK84798	Human cdn
36	1167	75.6	5407	4	ABL18530	CDNA enco
37	1167	75.6	8031	4	ABL20966	Drosophil
38	1167	75.6	8031	4	ABL20966	Drosophil
39	1165	75.5	1251	5	AAS79610	DNA encod
40	1137	73.7	1033	4	ABL03127	Drosophil
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44	1081	70.1	687	6	ABQ56282	Human ova
45	1043	67.6	3406	4	ABL03126	Drosophil

#### ALIGNMENTS

RESULT 1

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ID AAD00521 standard; cdna; 897 BP.

XX AAD00521;

AC AAD00521;

DT 29-AUG-2000 (first entry)

XX Human adenine nucleotide translocator ANT3 CDNA.

DE Human adenine nucleotide translocator ANT3 CDNA.

XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;  
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
KW mitochondrial permeability transition; neuroprotective; neurotoxic;  
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
KW myoclonic epilepsy red ragged fibre syndrome; ss.

XX Homo sapiens.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..897

FT /\*tag= a

FT /product= "ANT3"

XX WO200026370-A2.

PD 11-MAY-2000.

XX

PF 03-NOV-1999; 99WO-US025883.  
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 PR 03-NOV-1998; 98US-00185904.  
 PR 08-SEP-1999; 99US-00393441.  
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 XX (MITO-) MITOKOR.  
 PA  
 XX  
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW;  
 PI Szabo TR, Ghosh SS;  
 XX P-PSDB; AAY71033.  
 DR WPI: 2000-365619/31.  
 DR P-PSDB; AAY71033.  
 XX  
 PT Recombinant construct encoding adenine nucleotide translocator  
 PT polypeptide, useful e.g. in screening for potential therapeutic agents  
 PT against mitochondrial disease.  
 XX  
 PS Example 1; Page 166; 175pp; English.  
 XX  
 CC The patent discloses a method to produce adenine nucleotide translocator  
 CC (ANT) proteins or ANT fusion proteins using recombinant expression  
 CC constructs. ANT is a nuclear encoded protein and a major component of  
 CC inner mitochondrial membrane. It mediates transport of adenosine di/tri-  
 CC phosphates across the mitochondrial inner membrane and also serves as an  
 CC important molecular component of the mitochondrial permeability  
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
 CC or ligands that bind to, or interact with it. The ANT ligands are used to  
 CC detect or isolate ANT in a biological sample, and therapeutically for  
 CC regulating mitochondrial pore activity, for treating diseases associated  
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's  
 CC hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy,  
 CC lactic acidosis and stroke (MEAS), hyperproliferative disorders,  
 CC mitochondrial diabetes and deafness (MIDB), and myoclonic epilepsy red  
 CC ragged fibre syndrome. The present sequence is a cDNA encoding adenine  
 CC nucleotide translocator ANT3 from human brain  
 XX  
 SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 5.4e-172 Length: 897  
 Score: 1543.00 Matches: 298  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 3 Gaps: 0  
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 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnGlnHis 40  
 DB 61 ATCTCCAGACGGCGGTGGCTCCGATCGAGGGGTCAAGTGTCTGCTGCAAGGTCCAGCAC 120  
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
 DB 121 GCCAGCAGCAGATCGCGCGGCAACAGCAGTACAGGGCATCGTGGACTGCATGTGCCG 180  
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80  
 DB 181 ATCCCCAAGAGCAGCGCGTCTCTCTCTGAGGGGCAACCTTGCACACGTCATTCGC 240  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
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QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
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 DB 421 CTGGCAGCGGCGTGGAAAGTCAGGCACAGCGCGAGTTCGAGGCGCTGGAGACTGC 480  
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
 DB 481 CTGGTGAAGATCACCAAGTCCGACGGCATCGGGGCTGTACACAGGGCTTCAGTGTCTCC 540  
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 DB 541 GTGCAGGGCATCATCATCTACCGGCGGCTTCTTCCGCGTGTACGATACGCGCAAGGCGC 600  
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 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 DB 661 ACGGCGCGTGGCGCGGTGTCTCTTACCCCTTCGACACGGTGGCGGCGCATGATGATG 720  
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
 DB 721 CAGTCCGGCGGCAAGGAGCTGACATCATGTACAGGCGCACCGTCTGCTGTGGAGGAG 780  
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 DB 781 ATCTTCAGAGATGAGCGGGCGCAAGCCCTTCTCAAGGGTGGTGGTCCCAAGCTCTCTCGG 840  
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298  
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RESULT 2  
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 ID AAS05903 standard; cDNA; 897 BP.  
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 AC AAS05903;  
 XX  
 DT 07-SEP-2001 (first entry)  
 XX  
 DE Human adenine nucleotide translocator-3 (ANT-3) cDNA sequence.  
 XX  
 KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.  
 OS Homo sapiens.  
 PH Key Location/Qualifiers  
 FT CDS 1..897  
 FT /\*tag= a  
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 XX  
 PN WO200132876-A2.  
 XX  
 PD 10-MAY-2001.  
 XX  
 XX 03-NOV-2000; 2000WO-US030535.  
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 XX 03-NOV-1999; 99US-00434354.  
 PR  
 XX (MITO-) MITOKOR.  
 PA  
 XX Murphy AN, Clevenger W, Wiley SE, Andrejev AY, Frigeri LG;  
 PI Velicelebi G, Davis RE;  
 XX WPI; 2001-291054/30.  
 DR  
 DR P-PSDB; AAU01200.

xx CC The invention relates to a recombinant expression construct (I)  
CC comprising a regulated promoter operably linked to a nucleic acid  
CC encoding an adenine nucleotide translocator (ANT) polypeptide, ANT  
CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant

CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (i) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.  
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide,  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also  
 CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the coding sequence of human ANT3  
 XX

SQ Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 5.4e-172 Length: 897  
 Score: 1543.00 Matches: 298  
 Percent Similarity: 100.00% Conservations: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
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US-09-811-094-33 (1-298) x AAS16690 (1-897)

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Db	61	ATCTCCAGAGCGCGTGGTCCATCGAGCGGTCAAGTGTCTGCTGTCAGGTCACGAC	120
Qy	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
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Qy	61	IleProLysGluGlnGlyValLeuSerPheThrArgGlyValLeuAlaAsnValIleArg	80
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Qy	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
Db	601	ATGCTCCCGGACCCCAAGAACACGACATCTGTGTGAGCTGGATGATCGGCGACCGCTG	660
Qy	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet	240
Db	661	ACGGCGGTGGCGGCTGTCT	720

Qy	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys	260
Db	721	CAGTCCGCGCGCAAGGAGCTGACATCATGTACACGCGCACCGCTGCTGGAGGAAG	780
Qy	261	IlePheArgAspGluGlyValAlaPhePheLysGlyAlaTrpSerAsnValLeuArg	280
Db	781	ATCTTCAGAGATGAGGGGGGCGAGCCCTTCTCAAGGGTGGTGGTCCAGCTCTCGGG	840
Qy	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle	298
Db	841	GCGATGGGGGCGGCT	894

# RESULT 4

AA158797  
 ID AA158797 standard; cDNA; 1212 BP.

XX AA158797;

XX 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 1000.

Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 peripheral nervous system; neuropathy; central nervous system; CNS;  
 Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
 chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 leukaemia; ss.

OS Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-0052317.

XX 20-JUN-2000; 2000US-00538042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
 Zhou P, Goodrich R, Dermanac RT;

XX WPI: 2001-442253/47.

XX P-PSDB; AM39641.

XX Novel nucleic acids and polypeptides, useful for treating disorders such  
 as central nervous system injuries.

XX Claim 1; SEQ ID NO 1000; 10078pp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and the  
 encoded polypeptides (AAW38642-AAW42213) with neurotropic,  
 immunosuppressant and cytostatic activity. The polynucleotides are useful  
 in gene therapy. A composition containing a polypeptide or polynucleotide  
 of the invention may be used to treat diseases of the peripheral nervous  
 system, such as peripheral nervous injuries, peripheral neuropathy and  
 localized neuropathies and central nervous system diseases, such as  
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 utilisation of the activities such as: immune system suppression,  
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
 CC



CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: the sequence data for this patent did not form  
CC part of the printed specification

XX SQ Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,24e-172 Length: 1212  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x AAI58797 (1-1212)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20  
Db 131 ATGACGGAAACAGCCATCTCTTCCAAAGACTTCTTGGCGGAGGATCGCCGCC 190  
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
Db 191 ATCTCCAGACGGCGTGGCTCCGATCGAGGGTCAAGCTGCTGCGAGTCCAGCAC 250  
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
Db 251 GCCAGCAAGCAGATCGCCGCCACAGCAGTACAAGGGCATCTGCGATGTCGCGC 310  
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValleArg 80  
Db 311 ATCCCAAGGACGAGGGGTGTCTTCTGAGGGCAACCTTGGCCAAAGTTCATTCGC 370  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
Db 371 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAGGATAGTACAGCATCTTCTCTG 430  
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
Db 431 GGGGGCGTGGACAGACACAGCAGTCTGAGGTACTTGGCGGCAACCTGGCCTCGGC 490  
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
Db 491 GGTGGCGCGGGCGACCTCTCTCTGTTGTTACCCGCTGGATTTCCGCCAGAACCCGC 550  
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
Db 551 CTGGCAGCGGACGTGGAAAGTCAGGCACAGAGCGGAGTTCGAGGCGCTGGAGACTGC 610  
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
Db 611 CTGGTGAAGATCACCAAGTCCGACGGCATCCGGGGCCTGTACCAAGGGCTTCAGTGTCTCC 670  
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
Db 671 GTGCAGGGCATCATCATCTACGGGGCGGCTTCTTCCGCGTGTACGATACGCCCAAGGC 730  
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
Db 731 ATGCTCCCGACCCCAAGACAGCACATCATCTGTTGAGTGGATGATCGCGACCGGTG 790  
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
Db 791 ACGGCGCTGGCGGCGCTGTCTTCTTACCCCTTCACACGGTGGCGGCGCATGATGATG 850  
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
Db 851 CAGTCCGGCGCGCAAGGAGCTGACATCATGTACACGGGCACCGTCTGACTGTTGGAGGAG 910  
QY 261 IlePheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
Db 911 ATCTTCAGAGATAGGGGGGCAAGCCCTTCTTCAAGGGTGGCTGTCCAAAGCTCTCGCG 970  
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValle 298

Db 971 GGCAATGGGGGGCGCTTTCGTGCTGTACGAGCTCAAGAAGGTGATC 1024

RESULT 5

ADB48777  
ID ADB48777 standard; cDNA; 1212 BP.  
XX AC ADB48777;  
XX AC ADB48777;  
DT 04-DEC-2003 (first entry)  
XX DE Novel human cDNA SEQ ID NO 687.  
XX KW ss; cancer; neurodegenerative disease; human.  
XX OS Homo sapiens.  
FN US2003104529-A1.  
XX PD 05-JUN-2003.  
XX PF 04-JAN-2002; 2002US-00037270.  
XX PR 21-JAN-2000; 2000US-00488725.  
XX PR 25-APR-2000; 2000US-00552317.  
XX PR 19-JUL-2000; 2000US-00620312.  
XX PA (ZHOU)/ ZHOU P.  
PA (TANG)/ TANG Y T.  
PA (LIUC)/ LIU C.  
PA (ASUN)/ ASUNDI V.  
PA (DRMA)/ DRMANAC R T.  
XX PI Zhou P, Tang YT, Liu C, Asundi V, Drmanac RT;  
XX WFI; 2003-678194/64.

XX PT New polynucleotide, useful for treating diseases e.g., cancer or neurodegenerative diseases.  
XX PS Claim 1; SEQ ID NO 687; 99pp; English.  
XX CC The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030104529.  
XX SQ Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 8,24e-172 Length: 1212  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 8 Gaps: 0

US-09-811-094-33 (1-298) x ADB48777 (1-1212)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20  
Db 131 ATGACGGAAACAGCCATCTCTTCCAAAGACTTCTTGGCGGAGGATCGCCGCC 190  
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
Db 191 ATCTCCAGACGGCGTGGCTCCGATCGAGGGTCAAGCTGCTGCGAGTCCAGCAC 250  
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60

251 GCCAGCAGCAGATCGCGCGCGCACAGCAGTACCAAGGCGCATCGTGACTGCATTGTCCGC 310  
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyValLeuAlaAsnValIleArg 80  
Db 311 ATCCCCAAGGAGCGGGCTGCTCTCTTCGGAGGGCAACCTTGCCACGTCATTCGC 370  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100  
Db 371 TACTTCCCACTCAAGCCCTCAACTTCCCTTCAAGGATTAAGTACAAAGCAGATCTTCCTG 430  
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTrpPheAlaGlyAsnLeuAlaSerGly 120  
Db 431 GGGGCGCTGGACAAGCACACAGCTCTCGAGGTACTTTGCGGCAACCTGGGCTTCGGC 490  
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTrpProLeuAspPheAlaArgThrArg 140  
Db 491 GGTGCGCGCGCGGACCTCTCTCTGCTGTACCGCTGGATTTCGCCAGAACCCCGC 550  
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
Db 551 CTGGCAGCGGAGCTGGGAAAGTCAGGCACAGAGCGCGAGTTCCGAGGCTCGGAGACTGC 610  
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTrpGlnGlyPheSerValSer 180  
Db 611 CTGGTGAAGTACCAAGTCCAGCGGCATCCGCGGCTGTACCAAGGCTTCAGTGTCTCC 670  
QY 181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200  
Db 671 GTGCAGGCGCATCATCTACCGCGCGCCCTACTTCGCGGTACGATACGGCCCAAGGCG 730  
QY 201 MetLeuProAspProLysAsnHisIleValValSerTrpMetIleAlaGlnThrVal 220  
Db 731 ATGCTCCCGACCCCAAGAACACGCACATCGTGTGTAGCTGGATGTCGCGCAGACCGTG 790  
QY 221 ThrAlaValAlaGlyValValSerTrpPheAspThrValArgArgMetMetMet 240  
Db 791 ACGGCGTGGCGGCTGTCTCTACCTCCCTTCGACAGCGTGGCGGCGCGCATGATG 850  
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgLys 260  
Db 851 CAGTCCGGCGCGCAAGAGAGCTGACATCATGTACACGGCCCGCTGCTGTGAGGAAG 910  
QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
Db 911 ATCTTCAGAGATGAGGCGGGCAAGGCTCTTCAAGGGTGGTGTCTCAAGCTCTCGG 970  
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTrpAspGluLeuLysLysValIle 298  
Db 971 GGCATGGGGGGCGCTCTGCTGTCTGTCTGTACGACGAGCTCAAGAAGGTGATC 1024

## RESULT 6

AAI60583/c

ID AAI60583 standard; cDNA; 2035 BP.

XX AC

XX AA160583;

DT 22-OCT-2001 (first entry)

XX Human polynucleotide SEQ ID NO 4572.

DE Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;  
KW peripheral nervous system; neuropathy; central nervous system; CNS;  
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;  
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
KW leukaemia; ss.

XX OS Homo sapiens.

XX WO200153312-A1.

XX PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US034263.  
XX 23-DEC-1999; 99US-00471275.  
PR 21-JAN-2000; 2000US-00488725.  
PR 25-APR-2000; 2000US-00552317.  
PR 20-JUN-2000; 2000US-00598042.  
PR 19-JUL-2000; 2000US-00620312.  
PR 03-AUG-2000; 2000US-00653450.  
PR 14-SEP-2000; 2000US-00662191.  
PR 19-OCT-2000; 2000US-00693036.  
PR 29-NOV-2000; 2000US-00727344.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;  
PI Zhou P, Goodrich R, Drmanac RT;  
XX WPI: 2001-442253/47.  
DR P-PSDB; AAM411427.  
XX Novel nucleic acids and polypeptides, useful for treating disorders such  
PT as central nervous system injuries.  
XX Claim 1; SEQ ID NO 4572; 10078pp; English.  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the  
CC encoded polypeptides (AAM38642-AAM42123) with nootropic,  
CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
CC in gene therapy. A composition containing a polypeptide or polynucleotide  
CC of the invention may be used to treat diseases of the peripheral nervous  
CC system, such as peripheral nervous injuries, peripheral neuropathy and  
CC localised neuropathies and central nervous system diseases, such as  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
CC utilisation of the activities such as: immune system suppression,  
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,  
CC assays for receptor activity, arthritis and inflammation, leukaemias and  
CC C.N.S disorders. Note: The sequence data for this patent did not form  
CC part of the printed specification  
XX Sequence 2035 BP; 398 A; 611 C; 625 G; 401 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1-7e-171 Length: 2035  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x AAI60583 (1-2035)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAppPheLeuAlaGlyIleAlaAla 20  
Db 1932 ATGACGGAACAGCGCATCTCTTCGCAAGAGCTTCTTGGCGGAGGATCCGCCGCC 1873  
QY 21 IleSerLysThrAlaValAlaAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
Db 1872 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGGTCAAGCTGCTGTCAGGTCCAGCAC 1813  
QY 41 AlaSerLysGlnIleAlaAlaLysGlnTrpLysGlyIleValAspCysIleValArg 60  
Db 1812 GCCAGCAAGCAGATCGCCGCCGCAAGCAGTACAAAGGCGCATCTGTCGATGTCGCG 1753  
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80  
Db 1752 ATCCCCAAGGAGCAGGCGGTGCTGCTCTTCGAGGGGCAACCTTGGCAACGTCATTCG 1693  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100  
Db 1692 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAAGCAGATCTTCTCG 1633

QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
 Db 1632 GGGGGCGTGGCAAGACACAGCAGTCTCGAGTACTTTGGGGCAACCTGGCTCCGGC 1573  
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCySPheValTyrProLeuAspPheAlaArgThrArg 140  
 Db 1572 GTGGGGCGGGCGGACCTCTCTGCTTCCGCTACCCGCTGGATTTCCGAGAACCCGC 1513  
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
 Db 1512 CTGGCAGCGGACGTGGGAAGTCAAGCACAGAGCGGAGTTCCGAGGCTCGGAGACTGC 1453  
 QY 161 LeuValLysIleThrLysSerAspGlyLeuArgGlyLeuTyrGlnGlyPheSerValSer 180  
 Db 1452 CTGGTGAAGATCACCAGTCCGACGCGCATCCGGGGCCCTGTACCAAGGCTTCAGTGTCTCC 1393  
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
 Db 1392 GTGCAGGCGATCATCATCTACCGGGCGGCTTCTCGCGGTGACGATACGGCCAGGGC 1333  
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220  
 Db 1332 ATGCTCCCGGACCCCAAGACACGACATCGTGTGAGCTGATCGCGCAGACCGTG 1273  
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 Db 1272 ACGGCGGTGGCGGGCTGTGTCTTACCCCTTCGACAGGTGGCGGCGCATGATGATG 1213  
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
 Db 1212 CAGTCCGGCGGCAAGGAGCTGACATCATGTACACGGCCACCGTCTGACTGTGGAGGAAG 1153  
 QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
 Db 1152 ATCTTCAGATGAGGGGGGGAAGGCTTCTCAAGGGTGGTGGTCCCAACGTCCTCGCG 1093  
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298  
 Db 1092 GGCATGGGGGGCGCTTCGTGCTGCTCTGTACGACGAGCTCAAGAGGTGATC 1039  
 RESULT 7  
 ID ABX63152 standard; cDNA; 2592 BP.  
 AC ABX63152;  
 XX  
 DT 25-FEB-2003 (first entry)  
 XX  
 DE Human cDNA #152 differentially expressed in activated vascular tissue.  
 XX  
 DE Human; Gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;  
 KW hypotensive; antidiabetic; gynaecological; vasotrophic; cerebroprotective;  
 KW gene therapy; vascular disease; cancer; coronary; artery disease;  
 KW hypertension; diabetes; pre-eclampsia; restenosis;  
 KW ischaemia-reperfusion injury; stroke.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2002137081-A1.  
 XX  
 XX 26-SEP-2002.  
 PD  
 XX  
 PF 08-JAN-2002; 2002US-00044090.  
 XX  
 XX 28-JUL-2000; 2000US-0222469P.  
 PR 08-JAN-2001; 2001US-0260483P.  
 XX  
 XX (BAND/) BANDMAN O.  
 PA  
 XX Bandman O;  
 PI  
 XX WPI; 2003-110597/10.  
 DR

XX  
 PT Combination for diagnosing, staging, treating, or monitoring the  
 PT progression of treatment of a vascular disease, e.g. atherosclerosis,  
 PT comprises several cDNAs that are differentially expressed in activated  
 PT vascular tissue.  
 XX  
 PS Claim 1; Page; 18pp; English.  
 XX  
 CC This invention relates to a combination comprising several cDNAs that are  
 CC differentially expressed in activated vascular tissue. The invention also  
 CC discloses a high throughput method for detecting differentially expressed  
 CC cDNAs in a sample. The cDNAs of the invention may have  
 CC antiarteriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;  
 CC gynaecological; vasotrophic and cerebroprotective activities and may be  
 CC used in gene therapy. The cDNAs of the invention may be used in a high-  
 CC throughput methods for detecting differential expression of one or more  
 CC cDNAs in a sample, or screening several molecules or compounds to  
 CC identify a molecule or compound that specifically binds a cDNA of the  
 CC invention. A protein encoded by the cDNA may be used to screen several  
 CC molecules or compounds to identify a ligand that specifically binds to  
 CC the protein, or to produce or purify an antibody to the protein that can  
 CC be used to detect a protein in a sample or purify a natural or  
 CC recombinant protein from a sample. The nucleotides may be useful for  
 CC diagnosing, staging, treating, or monitoring the progression of treatment  
 CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery  
 CC disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion  
 CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale  
 CC genetic or gene expression analysis of several new nucleic acid  
 CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for  
 CC diagnosing pre-pathologic disorders, and chronic or acute diseases  
 CC associated with abnormalities in the expression, amount or distribution  
 CC of the protein. The present sequence represents a cDNA of the invention  
 CC that is differentially expressed in activated vascular tissue. Note: The  
 CC sequence data for this patent did not form part of the specification, but  
 CC was obtained in electronic format directly from USPTO at  
 CC http.segdata.uspto.gov/sequence.html?DocID=20020137081  
 XX  
 SQ Sequence 2592 BP; 520 A; 790 C; 766 G; 514 T; 0 U; 2 Other;

Alignment Scores:  
 Pred. No.: 1.86e-167 Length: 2592  
 Score: 1510.00 Matches: 296  
 Percent Similarity: 99.33% Conservative: 2  
 Best Local Similarity: 98.67% Mismatches: 0  
 Query Match: 97.86% Indels: 2  
 DB: 7 Gaps: 0

US-09-811-094-33 (1-298) x ABX63152 (1-2592)

Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIle-AlaAla 20  
 Db 207 ATGACGGAAACAGGCCATCTCTTCGCCAAAGACTTCTTGGCGGAGGCATGCGCCGCGC 266  
 Qy 20 alleSerLysThrAlaValAlaProIleGluArg-VallysLeuLeuLeuGlnValGlnH 40  
 Db 267 CATCTCCAAAGACGGCGGTGCGTCCGATCGAGGGGGTCAAGCTGCTGCTGAGGTCACG 326  
 Qy 40 isAlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValA 60  
 Db 327 ACCGACGACAGCAGATCGCGCGCAGAGGCTACAGGGCATCGTGGACTGCATTGTCC 386  
 Qy 60 rgIleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleA 80  
 Db 387 GCATCCCAAGGAGCAGGGCGTGTCTCTCTGGAGGGGCAACCTTGGCAAGTCATTTC 446  
 Qy 80 rgTyrPheProThrGlnAlaLeuAspPheAlaPheLysAspLysValTyrLysGlnIlePhe 100  
 Db 447 GCTACTTCCCACTCAAGCCCTCACTTCGCCCTCAAGGATTAAGTACACAGCAGATCTTC 506  
 Qy 100 euGlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerG 120  
 Db 507 TGGGGGGCGTGGACAAGCACACGACAGTCTTCTGAGGTACTTTGCGGGCAACCTGGCTCCG 566



Db 489 CTAGCAGCTGATGGTGGTAAAGCTGGAGCTGAAGGGAATTCGAGGCTCGGTGACTGC 548  
QY 161 LeuValLysIleThrLysSerAspGlyLeuArgGlyLeuTyrGlnGlyPheSerValSer 180  
Db 549 CTGGTTAAGATACAAATCTCATGGGATTAAGGGCTGTACCAAGGCTTTAAAGCTGTCT 608  
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
Db 609 GTGCAGGATATTATCATCTACCGAGCGGCTTCTCGGTATCTATGACACTGCAAGGGA 668  
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
Db 669 ATGCTTCGGGATCCCAAGAACACTCACATCGTCATCGTCATCGTCATCGTCATCGTC 728  
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValAlaArgArgMetMet 240  
Db 729 ACTGCTGTGCGGGTGTGACTTCCATTCATTTGACCGCTTCGCGCGGCGATGATG 788  
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
Db 789 CAGTCAGGCGCAAGGAACCTGACATCATGTACACAGGCACGCTTGACTGTGGCGGAAG 848  
QY 261 IlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
Db 849 ATTGCTCGTGATGAAGGAGGCAAGCTTTTTCAGGGTGTGATGTCCTCAATGTTCTCAGA 908  
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
Db 909 GCATGGTGGTGCTTTGTGCTTCTTGTATGATGAATCAGAGAG 956

RESULT 9  
AAD00520  
ID AAD00520 standard; cDNA; 897 BP.  
AC  
XX AAD00520;  
XX  
DT 29-AUG-2000 (first entry)  
XX  
DE Human adenine nucleotide translocator ANT2 cDNA.  
XX  
KW Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;  
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;  
KW mitochondrial permeability transition; neuroprotective; nontropic;  
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;  
KW antipsychotic; neuroprotective; therapeutic; screening; psoriasis;  
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;  
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;  
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;  
KW mitochondrial diabetes and deafness; hyperproliferative disorder;  
KW myoclonic epilepsy red ragged fibre syndrome; ss.

OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 1..897  
XX FT /\*tag= a  
XX FT /product= "ANT2"  
XX  
XX WO2000026370-A2.  
XX  
XX PD 11-MAY-2000.  
XX  
XX PF 03-NOV-1999; 99WO-US025883.  
XX  
XX PR 03-NOV-1998; 98US-00185904.  
XX PR 08-SEP-1999; 99US-00393441.  
XX  
XX XX (MITO-) MITOKOR.  
XX  
XX PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW;  
XX PI Szabo TR, Ghosh SS;

DR WPI; 2000-365619/31.  
DR P-PSDB; AAY1032.  
XX  
PT Recombinant construct encoding adenine nucleotide translocator  
PT polypeptide, useful e.g. in screening for potential therapeutic agents  
PT against mitochondrial disease.  
XX  
XX Example 1; Page 165-166; 175pp; English.  
XX  
CC The patent discloses a method to produce adenine nucleotide translocator  
CC (ANT) proteins or ANT fusion proteins using recombinant expression  
CC constructs. ANT is a nuclear encoded protein and a major component of  
CC inner mitochondrial membrane. It mediates transport of adenosine di/tri-  
CC phosphates across the mitochondrial inner membrane and also serves as an  
CC important molecular component of the mitochondrial permeability  
CC transition pore, a modulator of apoptosis. ANT is used to identify agents  
CC or ligands that bind to, or interact with it. The ANT ligands are used to  
CC detect or isolate ANT in a biological sample, and therapeutically for  
CC regulating mitochondrial pore activity, for treating diseases associated  
CC with altered mitochondrial function, including Alzheimer's, Parkinson's  
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia, Leber's  
CC hereditary optic neuropathy, schizophrenia, mitochondrial encephalopathy,  
CC lactic acidosis and stroke (MELAS), hyperproliferative disorders,  
CC mitochondrial diabetes and deafness (MIDD), and myoclonic epilepsy red  
CC ragged fibre syndrome. The present sequence is a cDNA encoding adenine  
CC nucleotide translocator ANT2 from human brain  
XX  
SQ Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.69e-161 Length: 897  
Score: 1454.00 Matches: 274  
Percent Similarity: 96.96% Conservative: 13  
Best Local Similarity: 92.57% Mismatches: 9  
Query Match: 94.23% Indels: 0  
DB: 3 Gaps: 0

US-09-811-094-33 (1-298) x AAD00520 (1-897)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20  
Db 1 ATCAGCAGATCCCGCATTTGCTTCGCCAAGGACTTCTGCGAGGTGGATGCCGAGGCC 60  
QY 21 IleSerLysThrAlaValAlaProfileGluArgValLysLeuLeuGlnValGlnHis 40  
Db 61 ATCTCCAAGCGCGGTAGCGGCATCGAGCGGTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
Db 121 GCCAGCAGCAGATCACTGCAGATAGCAATCAAGGCATTTATGACTGCGGTGCTGCT 180  
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80  
Db 181 ATTCCCAAGGAGCAGGAGTTCCTCTCTTCTGCGCGGTAACTGGCCCAATGTCATCAGA 240  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
Db 241 TACTTCCCGCAGCGCTCTTAACCTCGCTTCAAGAGTAAATACAGCAGATCTTCTCTG 300  
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
Db 301 GGTGGTGTGCAACAAGAGAACCCAGTTTGGCCCTACTTTCAGGGAATCTGCAATCGGT 360  
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
Db 361 GGTGCGCAGGCGCCACATCCCTGTGTTTGTGTACCTCTTGTATTTGCCCGTACCCGT 420  
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
Db 421 CTAGCAGCTGATGTGGGTAAAGCTGAGCTGAAGGAATTCGAGGCTCTCGGTGACTGC 480  
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180

DB 481 CTGGTTAAGATCTACAAATCTGATGGGTAATAGGGCCCTGTACCAAGGCTTTAACTGTCT 540  
 QY 181 ValGlnGlyllellelleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
 DB 541 GTGCAGGGTATTATCATCTACCGAGCCGCTTACTTCGGTATCTATGACATCTGCAGAGGGA 600  
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220  
 DB 601 ATGCTTCGGATCCCAAGACACTCATCGTCATCAGCTGGATGTCGACAGCTGTC 660  
 QY 221 ThrAlaValAlaGlyValValSerTyrPropheAspThrValArgArgMetMetMet 240  
 DB 661 ACTGCTGTTCGGGTTGACTTCTCATTCATTTGACACCGCTTGCCTCCGATGATG 720  
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260  
 DB 721 CAGTCAGGCGCAAGGAACCTGACATCATGTACACAGCGCTTGACTGCTGGCGAAG 780  
 QY 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTyrPheAsnValLeuArg 280  
 DB 781 ATTGCTGCTGATGAAGGAGGCAAGCTTTTTCAGGGTGCATGTCATGTTCTCAGA 840  
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
 DB 841 GGCATGGGTGGTGTCTTTGTGCTTGTCTGTATGATGAAATCAAGAAG 888

RESULT 10  
 AAS05902  
 ID AAS05902 standard; cDNA; 897 BP.  
 AC AAS05902;  
 DT 07-SEP-2001 (first entry)  
 DE Human adenine nucleotide translocator-2 (ANT-2) cDNA sequence.  
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;  
 KW mitochondrial permeability transition pore component; cell survival;  
 KW mitochondrial core component; mitochondrial related disorder; cancer;  
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.  
 OS Homo sapiens.  
 FH Key  
 FT CDS  
 FT Location/Qualifiers  
 FT 1..897  
 FT /\*tag= a  
 FT /product= "ANT-2"  
 PN WO200132876-A2.  
 XX 10-MAY-2001.  
 PF 03-NOV-2000; 2000WO-US030535.  
 PR 03-NOV-1999; 99US-00434354..  
 XX (MITO-) MITOKOR.  
 PA Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;  
 PI Velicelebi G, Davis RE;  
 XX WPI: 2001-291054/30.  
 DR P-PSDB; AAU01199.  
 XX New nucleic acid expression constructs, useful for screening for agents  
 PT that alter mitochondrial permeability transition (MPT), comprises  
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide fused  
 PT to energy transfer molecule.  
 XX Disclosure; Fig 1; 186pp; English.  
 PS The present sequence encodes for human adenine nucleotide translocator-2  
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability transition

CC (MTP) pore components responsible for mediating transport of ADP across  
 CC the mitochondrial inner membrane. ANT proteins interact with other  
 CC mitochondrial core components e.g. cyclophilins to regulate MPT. The  
 CC present invention relates to a novel nucleic acid expression construct  
 CC comprising a promoter operably linked to a polynucleotide encoding a  
 CC mitochondrial pore component polypeptide (e.g. ANT) fused to an energy  
 CC transfer molecule (ETM) protein (e.g. green fluorescent protein (GFP) or  
 CC a FLASh sequence). The novel expression construct can alter mitochondrial  
 CC membrane permeability transition and/or alter the interaction between  
 CC mitochondrial core components. The methods are useful for screening for  
 CC agents that alter MPT and/or cell survival. These agents are useful for  
 CC the prevention or treatment of diseases associated with altered  
 CC mitochondrial function or dysfunctional cell survival, such as  
 CC Alzheimer's disease, diabetes mellitus, Parkinson's disease, Huntington's  
 CC disease, schizophrenia, mitochondrial encephalopathy, lactic acidosis,  
 CC stroke, hyperproliferative disorders e.g. cancer, and deafness  
 XX Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.69e-161 Length: 897  
 Score: 1454.00 Matches: 274  
 Percent Similarity: 96.96% Conservative: 13  
 Best Local Similarity: 92.57% Mismatches: 9  
 Query Match: 94.23% Indels: 0  
 DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x AAS05902 (1-897)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla 20  
 DB 1 ATGCACAGATGCCGCAATTGCTTCCCAAGACTTCTCGGAGGTGGAGTGGCGCAGCC 60  
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
 DB 61 ATCTCCAGACGGCGGTAGCGCCCATCGAGCGGGTCAAGCTGCTGCTCGAGTGCAGCAT 120  
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
 DB 121 GCCACAGACAGATCACTGCAGATGAAGCAATACAAAGCAATTATAGACTGGTGGTCCGT 180  
 QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80  
 DB 181 ATTCCNAGGACGACGAAAGTTCTGCTCTTGGCGCGTAACTGGCCAAATGTATCAGA 240  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
 DB 241 TACTTCCCAAGGCTCTTAACATTCGCTTCAAGGATTAATACAGCAATCTCTCTG 300  
 QY 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
 DB 301 GGTGGTGGACAGAGAACCCAGTTTGGCGCTACTTTGCAGGCAATCTGGCATCGGT 360  
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
 DB 361 GGTGGCGCAGGGGCCACATCCCTGTGTTTGTGTACCTCTTGATTTTGGCCGACCCGT 420  
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
 DB 421 CTAGCAGCTGATGTGGTAAAGCTGGAGCTGAAGGGAATCCGAGGCTCGGTGACTGC 480  
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
 DB 481 CTGTTAAGATCTCAAAATCTCATGGATTAAAGGCGCTGTACCAAGGCTTTAACTGTCT 540  
 QY 181 ValGlnGlyllellelleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
 DB 541 GTGCAGGGTATTATCATCTACCGAGCCGCTTACTTCGGTATCTATGACATCTGCAGAGGGA 600  
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220  
 DB 601 ATGCTTCGGATCCCAAGGAACACTCACATCGTCATCAGCTGGATGATCGCACAGACTGTC 660

QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 Db 661 ACTGCTGTTGCCGGGTGACTTCTCATCCATTGACACCGTTTCGCCGCGCATGATGATG 720  
 QY 241 GlnSerGlyValGlyValAlaAspMetTyrThrGlyThrValAspCysTrpArgLys 260  
 Db 721 CAGTCAGGCGGCAAGAACTGACATCATGTCACACAGGACCGTTGACTGCTGCGGGAAG 780  
 QY 261 IlePheArgAspGluGlyValAlaPhePheLysGlyValAlaTrpSerAsnValLeuArg 280  
 Db 781 ATTGCTCGTGATCAAGAGGCAAGCTTTTCAAGGGTGCGATGCTCCAATGTTCTCAGA 840  
 QY 281 GlyMetGlyGlyValAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
 Db 841 GGCATGGGTGGTCTTTTGCTTGCTTGATGATGAATCAAGAAG 888

## RESULT 11

AAS16689

ID AAS16689 standard; cDNA; 897 BP.

XX AAS16689;

DT 14-FEB-2002 (first entry)

XX DNA encoding human adenine nucleotide translocator 2 (ANT2).

XX Human; adenine nucleotide translocator; ANT; ss;  
 KW mitochondrial matrix protein.

XX Homo sapiens.

XX Key Location/Qualifiers

FH 1..897

FT /\*tag= a

FT /product= "Adenine nucleotide translocator 2 (ANT2)";

XX WO200185944-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-US015416.

XX 11-MAY-2000; 2000US-00569327.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW;

PI Szabo TR, Ghosh SS, Moos WH, Pei Y, Carroll AK;

XX WPI; 2002-055598/07.

DR P-PSDB; AAU10379.

XX Novel recombinant expression construct for producing adenine nucleotide  
 PT translocator polypeptides, comprises a regulated promoter linked to  
 PT nucleic acid encoding the polypeptide.

XX Example 1; Fig 1; 147bp; English.

XX The invention relates to a recombinant expression construct (I)  
 CC comprising a regulated promoter operably linked to a nucleic acid  
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT  
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial  
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant  
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and  
 CC culturing the host cell. (I) is also useful for targeting a polypeptide  
 CC of interest to a mitochondrial membrane, where ANT polypeptide is  
 CC expressed as a fusion protein with the polypeptide of interest.

XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is  
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT  
 CC ligand is useful for determining the presence of an ANT polypeptide.  
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating  
 CC ANT from a biological sample, where the ANT ligand is covalently or non-  
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also

CC useful for identifying an agent that interacts with an ANT polypeptide.  
 CC The present sequence represents the coding sequence of human ANT2

SQ Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.69e-161 Length: 897  
 Score: 1454.00 Matches: 274  
 Percent Similarity: 96.96% Conservative: 13  
 Best Local Similarity: 92.57% Mismatches: 9  
 Query Match: 94.23% Indels: 0  
 DB: 6 Gaps: 0

US-09-811-094-33 (1-298) x AAS16689 (1-897)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaA 20  
 Db 1 ATGACAGATCCGCGATGTCTTCGCCAAGGATTTCTGGCAGGTGGAGTGGCGGAGCC 60  
 QY 21 IleSerLysThrAlaValAlaProlleGluArgValLysLeuLeuGlnValGlnHis 40  
 Db 61 ATCTCCAAGACGGCGGTAGCGCCATCGAGCGGTCAGCTGCTGCTGCAGGTGCAGCAT 120  
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
 Db 121 GCCAGCAGCAGATCACTGCAGATAGCAATACAAAGGCAATATAGACTGCGTGGTCCGT 180  
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80  
 Db 181 ATTCCCAAGGACGAGGAAGTTCTGTCCTTCGCGCGGTAACTGGCCCAATGTCATCAGA 240  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
 Db 241 TACTTCCCCACCCAGGCTCTTAACTTCGCCCTTCAAGAGATAAATACAAAGCAGATCTTCTTG 300  
 QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
 Db 301 GGTGGTGTGGACAGAGAACCCAGTTTGGCGCTACTTTGCAGGGGAATCTGGCATCGGGT 360  
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
 Db 361 GGTGGCGCAGGGGCCACATCCCTGTGTTTGTGTACCTCTTGATTTTCCCGTACCCGT 420  
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
 Db 421 CTAGCAGCTGATGTGGTAAAGCTGGAGCTGAAGGGAATTCGAGGCTTCGGTGACTGC 480  
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
 Db 481 CTGTTTAAGATCTACAAATCTGATGGATTAAAGGCCCTGTACCAGGCTTTAACGTGTCT 540  
 QY 181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200  
 Db 541 GTGCAGGGTATTATCATCTACCGAGCCGCTACTTTCGGTATCTATGACACTGCAAGGGA 600  
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220  
 Db 601 ATGCTTCCGATCCCAAGAACACTCACATCGTCATCAGCTGGATGATGCCAGACTGTC 660  
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgArgMetMetMet 240  
 Db 661 ACTGCTGTTTGGCGGGTGTACTTCTCATCATTTGACACCGCTTCGCCGCGCATGATGATG 720  
 QY 241 GlnSerGlyValGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
 Db 721 CAGTCAGGCGGCAAGAACTGACATCATGTCACAGGACCGCTTGACTGCTGGCGGGAAG 780  
 QY 261 IlePheArgAspGluGlyValLysAlaPhePheLysGlyValAlaTrpSerAsnValLeuArg 280  
 Db 781 ATTGCTCGTGATCAAGAGGCAAGCTTTTCAAGGGTGCGATGCTCCAATGTTCTCAGA 840  
 QY 281 GlyMetGlyGlyValAlaPheValLeuValLeuTyrAspGluLeuLysLys 296



Db	841	GGCATGGGGTGGCTTTTGTGCTTCTGTATGATGAATCAAGAAG	889
RESULT 12			
ABK63420			
ID	ABK63420	standard; cDNA; 1196 BP.	
AC	XX		
AC	XX		
XX	ABK63420;		
DT	18-JUN-2002	(first entry)	
XX	XX		
DE	XX	Rat sequence differentially expressed in response to a hepto-	
XX	XX	toxin; ss; hepatotoxin; expressed sequence tag; EST; drug screen-	
KW	KW	differential expression; centrilobular necrosis; steatosis.	
KW	XX		
OS	Rattus norvegicus.		
XX	XX		
PN	WO200210453-A2.		
XX	XX		
PD	07-FEB-2002.		
XX	XX		
PF	30-JUL-2001; 2001WO-US023872.		
XX	XX		
PR	31-JUL-2000; 2000US-0222040P.		
PR	02-NOV-2000; 2000US-0244880P.		
PR	11-MAY-2001; 2001US-0290029P.		
PR	15-MAY-2001; 2001US-0290645P.		
PR	22-MAY-2001; 2001US-0292336P.		
PR	06-JUN-2001; 2001US-0295798P.		
PR	13-JUN-2001; 2001US-0297457P.		
PR	19-JUN-2001; 2001US-0298884P.		
PR	09-JUL-2001; 2001US-0303459P.		
XX	XX		
PA	(GENE-)	GENE LOGIC INC.	

CC characterised by centrilobular necrosis and steatosis. The present  
CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene  
CC which is differentially expressed in response to a hepatotoxic agent  
XX  
SQ Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 8,73e-158 Length: 1196  
Score: 1424.00 Matches: 267  
Percent Similarity: 95.64% Conservative: 18  
Best Local Similarity: 89.60% Mismatches: 13  
Query Match: 92.29% Indels: 0  
DB: Gaps: 0

US-09-811-094-33 (1-298) x ABK63420 (1-1196)

QY	1	MetThrGluGlnAlaIleSerPheAlaLysASPheLeuAlaGlyGlyIleAlaAla 20
DB	76	ATGGGGGATCAGGCTTTGAGCTTCCTTAAGGACTTCCTGGCAGGTGGCATCCGCCGCC 133
QY	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB	136	GTCTCCAAAGACCGGGTCCGCCGATCAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 195
QY	41	AlaSerLysGlnIleAlaAlaASPheLysGlnTyrLysGlyIleValASPcysIleValArg 60
DB	196	GCCAGCAACAGATCAGTCGACGAGAGAAACAGTACAAAGGCATCATTTGTTGCTGTGAGA 255
QY	61	IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaasnValIleArg 80
DB	256	ATCCCCAAAGGACGAGGGCTTCTCTCCCTCTGAGGGGTAACTGCGCAACGTGATCCGG 315
QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB	316	TACTTCCCAACCCAGACTCTCACTTGCCTTCAGGACAGGTACAAAGCAGATCTTCCTG 375
QY	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB	376	CGAGGTGTGGATCGTCATAAAGCAGTTCTGCGCGTACTTCGCTGGTAACTGCGCTCTGT 435
QY	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuASPheAlaArgThrArg 140
DB	436	GGGGCAGCTGGGGCTTACCTCCCTCTGCTTCTGTCACCCACTGACATTGCTAGGACCCAG 495
QY	141	LeuAlaAlaASPValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyASPcys 160
DB	496	CTGGCTCCGACGTGGCGCAAGGGATCTCCACAGCGTAGTTCAATGGGTGGGTGACTGT 555
QY	161	LeuValLysIleThrLysSerASPcylIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB	556	CTCACCAAGATCTCAAGTCTGATGGGCTGAAGGGTCTCTACCAGGGTTTCAGTGTCCT 615
QY	181	ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrASPThrAlaLysGly 200
DB	616	GTCGAGGCAATCATCATCTACAGAGCTGCCTACTTCGGAGTCTATGACACTGCCAAGGG 675
QY	201	MetLeuProASPProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB	676	ATGCTGCCACAGCCCCAAGAATGTGCATATTATGTGTAGCTGGAGTATGCCCAGAGTGG 735
QY	221	ThrAlaValAlaGlyValValSerTyrProPheASPThrValArgArgMetMetMet 240
DB	736	ACAGCCGTGGCGGGGCTGGTCTCTATCCATTTGACACTGCTCGTGTAGGATGATGATG 795
QY	241	GlnSerGlyArgLysGlyAlaASPileMetTyrThrGlyThrValASPcysTrpArgLys 260
DB	796	CAGTCTGGCCGCGAAAGGGCTCATATTATGTATACACGGGGACAGTTGACTGCTGGAGGAG 855
QY	261	IlePheArgASPcylGlyGlyAlaPhePheLysGlyValATrpSerAsnValLeuArg 280
DB	856	ATTGCCAAAGATGAAGGACGCAAGACTTTCTTCAAGGTGCTTGGTCCCAACGTACTGAGA 915
QY	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrASPcylLeuLysLysValIle 298



916 GGCAAGGGGGGCTTTTGGTATGGTATGATGAGATCAAAAAATATGTG 969

Db

RESULT 13  
ADBS7820  
ID ADBS7820 standard; DNA; 1196 BP.  
XX AC ADBS7820;  
XX AC  
XX AC  
DT 04-DEC-2003 (first entry)  
XX  
XX Toxicity-related gene, SEQ ID 2846.  
XX DE  
XX DE  
KW toxin; gene expression profile; hepatotoxicity; liver;  
KW screening; toxicity assay; ds.  
XX  
XX  
XX Unidentified.  
XX OS  
XX PN WO2003064624-A2.  
XX XX  
XX PD  
XX PD  
XX PD  
XX PF 31-JAN-2003; 2003WO-US003194.  
XX XX  
XX PR 31-JAN-2002; 2002US-00060087.  
XX PR 15-MAR-2002; 2002US-0364045P.  
XX PR 15-MAR-2002; 2002US-0364055P.  
XX PR 30-DEC-2002; 2002US-0436654P.  
XX XX  
XX XX  
XX PA (GENE-) GENE LOGIC INC.  
XX XX  
XX PI Mendrick D, Porter M, Johnson K, Higgins B, Castle A, Elashoff M;  
XX DR WPI; 2003-689530/65.  
XX XX  
XX PT Predicting a toxic effect of a compound, useful in identifying toxicity  
XX PT markers in liver tissues or cells for drug screening and toxicity assays;  
XX PT comprises preparing gene expression profile of tissue or cells exposed to  
XX PT the compound.  
XX XX  
XX PS Claim 1; SEQ ID NO 2846; 1156pp; English.  
XX XX  
XX CC The present invention relates to a method for predicting a toxic effect  
XX CC of a compound. The method comprises preparing a gene expression profile  
XX CC of a tissue or cell sample exposed to the compound, and comparing the  
XX CC gene expression profile to a database comprising SEQ ID 1-4925, where  
XX CC differential expression of the gene indicates at least one toxic effect.  
XX CC The method is useful for predicting at least one toxic effect of a  
XX CC compound, predicting hepatotoxicity or the progression of a toxic effect  
XX CC of a compound, identifying an agent that modulates the onset or  
XX CC progression of a toxic response, predicting the cellular pathways that a  
XX CC compound modulates in a cell, and identifying an agent that modulates at  
XX CC least one activity of a protein. The method and compositions of the  
XX CC present invention using a database of genes having liver toxin-induced  
XX CC differential expression, are useful in identifying toxicity markers in  
XX CC liver tissues or cells for drug screening and toxicity assays. Note: The  
XX CC sequence data for this patent did not form part of the printed  
XX CC specification, but was obtained in electronic format directly from WIPO  
XX CC at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).  
XX XX  
SQ Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 U; 0 Other;  
XX XX

Alignment Scores:  
Pred. No.: 8,73e-158 Length: 1196  
Score: 1424.00 Matches: 267  
Percent Similarity: 95.64% Conservative: 18  
Best Local Similarity: 89.60% Mismatches: 13  
Query Match: 92.29% Indels: 0  
DB: 9 Gaps: 0

US-09-811-094-33 (1-299) x ADBS7820 (1-1196)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla 20

OS Rattus norvegicus.  
 XX WO2003065993-A2.  
 PN 14-AUG-2003.  
 PD 04-FEB-2003; 2003WO-US003482.  
 PF 04-FEB-2002; 2002US-0353171P.  
 PR 13-MAR-2002; 2002US-0363534P.  
 PR 08-APR-2002; 2002US-0370248P.  
 PR 10-APR-2002; 2002US-0371134P.  
 PR 10-APR-2002; 2002US-0371135P.  
 PR 10-APR-2002; 2002US-0371150P.  
 PR 11-APR-2002; 2002US-0371413P.  
 PR 19-APR-2002; 2002US-0373601P.  
 PR 19-APR-2002; 2002US-0373602P.  
 PR 22-APR-2002; 2002US-0374139P.  
 PR 08-MAY-2002; 2002US-0378370P.  
 PR 09-MAY-2002; 2002US-0378652P.  
 PR 09-MAY-2002; 2002US-0378653P.  
 PR 09-MAY-2002; 2002US-0378665P.  
 PR 09-JUN-2002; 2002US-0384230P.  
 PR 09-JUL-2002; 2002US-0394253P.  
 PR 04-SEP-2002; 2002US-0407688P.  
 PR 28-JAN-2003; 2003US-0442900P.  
 XX (GENE-) GENE LOGIC INC.  
 XX Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;  
 PI Elashoff M;  
 XX WPI; 2003-731472/69.  
 XX  
 PT Determining if a compound induces a toxic effect on a tissue or cell, for  
 PT identifying hepatotoxic compounds, comprises comparing a gene expression  
 PT profile of a tissue or cell sample to a database of Tox mean and non-Tox  
 PT mean values.  
 XX  
 PS Claim 44; SEQ ID NO 2883; 874pp; English.  
 XX  
 CC The present invention describes a method for determining whether a  
 CC compound induces a toxic effect on a tissue or cell. The method comprises  
 CC preparing a gene expression profile of a tissue or cell sample exposed to  
 CC the compound, and comparing the gene expression profile to a database  
 CC comprising data or information on the Tox mean and non-Tox mean value.  
 CC The method is useful for predicting or identifying at least one toxic  
 CC effect, particularly hepatotoxicity, of a test or unknown compound. The  
 CC genes listed in the specification are useful as diagnostic or toxicity  
 CC markers for the prediction or identification of the physiological state  
 CC of tissue or cell sample that has been exposed to a compound, or to  
 CC identify or predict the toxic effects of a compound or an agent. These  
 CC may also be used as markers for monitoring toxicity progression or for  
 CC drug screening. The present sequence represents a primary rat hepatocyte  
 CC toxicity modelling related gene sequence from the present invention.  
 XX  
 SQ Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 9.73e-158 Length: 1196  
 Score: 1424.00 Matches: 267  
 Percent Similarity: 95.64% Conservativity: 18  
 Best Local Similarity: 89.60% Mismatches: 13  
 Query Match: 92.29% Indels: 0  
 DB: 9 Gaps: 0  
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 Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnHis 40

Db 136 GTCTCCAAGACCGCGGTGCGCCCGATGAGAGGGTCAAACTGCTGTCAGGTCACGAT 195  
 Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnIleValAspCysIleValArg 60  
 Db 196 GCCAGCAACAGATCAGTGCAGAGAAACAGTACAAAGGCATCATTTGTTGTCGAGA 255  
 Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80  
 Db 256 ATCCCAAGGAGCAGGGCTTTCTCTCTCTGAGGGGTAACTGGCCCAACGATCCGG 315  
 Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
 Db 316 TACTTCCCCACCCCAAGCTCTCACTTGGCTTCAAGGACAAAGTACAGCAGATTTCTG 375  
 Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
 Db 376 GGAGGTGGATCGTCATACAGCAGTTCTGGCGCTACTTCGCTGAACCTGGCCTCTGT 435  
 Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
 Db 436 GGGGAGCTGGGGCTACCTCTCTCTCTTACCCACTGGACTTGTAGACCAAGG 495  
 Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
 Db 496 CTGGCTGCCGACGTGGGCAAGGATCTTCCAGAGCTGAGTTCAATGGGCTGGTACTGT 555  
 Qy 161 LeuValLysIleThrLysSerAspGlyIleArgLysGlyLeuTyrGlnGlyPheSerValSer 180  
 Db 556 CTCACCAAGATCTTCAAGTCTGATGGCTGAAGGGTCTCTACACAGGGTTTCAGTGTCTCT 615  
 Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaIleTyrPheGlyValTyrAspThrAlaLysGly 200  
 Db 616 GTGCAGGCGATCATCATCTACAGAGCTGCTTCTGGAGTCTATGACACTGCCAAGGGG 675  
 Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
 Db 676 ATGCTCCAGACCCCAAGATGTGCACATTATTGTGAGCTGGATGATTCGCCAGATGTG 735  
 Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 Db 736 ACAGCGGTGGCGGGCTGCTGCTATCCATTGACACTGTCCTGCTGAGATGATGATG 795  
 Qy 241 GlnSerGlyArgLysGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
 Db 796 CAGTCTGCCGGAAGAGGGGCTGATATATGATACACGGGACAGTTGACTGCTGGAGGAAG 855  
 Qy 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
 Db 856 ATTGCAAAAGATGAAGGACGCAAAAGCTTCTTCAAAGGTGCTTGGTCCAACTACTGAGA 915  
 Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298  
 Db 916 GGCATGGGGGGTGGCTTTTGTATTGATGATGATGATGATGATGATGATGATG 969

RESULT 15  
 ACC46652  
 ID ACC46652 standard; cDNA; 2213 BP.  
 XX ACC46652;  
 AC ACC46652;  
 XX  
 DT 02-JUN-2003 (first entry)  
 XX  
 DE Human dithp organelle-associated protein-encoding cDNA.  
 XX  
 XX Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antinease therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW organelle-associated protein; gene; ss.

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XX OS Homo sapiens.
XX PN WO200297031-A2.
XX PD 05-DEC-2002.
XX PF 27-MAR-2002; 2002WO-US010056.
XX PR 28-MAR-2001; 2001US-0279619P.
XX PR 29-MAR-2001; 2001US-0280067P.
XX PR 29-MAR-2001; 2001US-0280068P.
XX PR 16-MAY-2001; 2001US-0291280P.
XX PR 17-MAY-2001; 2001US-0291829P.
XX PR 17-MAY-2001; 2001US-0291849P.
XX PR 19-JUN-2001; 2001US-0299428P.
XX PR 20-JUN-2001; 2001US-0299776P.
XX PR 20-JUN-2001; 2001US-0300001P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason C, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David WH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
XX WPI; 2003-129518/12.
DR P-PSDB; ABR41715.
XX
XX Novel human diagnostic and therapeutic polypeptide useful for identifying
XX test compound which specifically binds to a polypeptide encoded by human
XX diagnostic and therapeutic polynucleotide, and to induce antibodies.
XX
XX Claim 2; SEQ ID NO 573; 591pp; English.
XX
XX The invention relates to novel human diagnostic and therapeutic
XX polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded
XX proteins (DITHP; ABR41136-ABR41812). The invention also relates to
XX polynucleotide sequences at least 90% identical to the dithp cDNA
XX sequences of the invention; recombinant vectors, host cells and
XX transgenic organisms comprising a dithp nucleic acid sequence; the
XX recombinant production of DITHP proteins; antibodies specific for DITHP
XX proteins; microarrays comprising dithp nucleic acid sequences; methods of
XX detecting dithp nucleotide and protein sequences; methods of screening
XX for compounds which specifically bind a DITHP protein; and methods of
XX assessing the toxicity of test compounds using a dithp hybridisation
XX probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
XX diagnosis of a wide variety of conditions including cancer and other cell
XX proliferative disorders; autoimmune or inflammatory disorders; bacterial,
XX viral, fungal or parasitic infections; hormonal disorders; metabolic
XX disorders; neurological disorders; gastrointestinal disorders; transport
XX disorders; and connective tissue disorders. They may also be used to
XX screen for modulators of protein activity or gene expression. DITHP
XX proteins can additionally be used in analysis of the proteome of a tissue
XX or cell type and to induce antibodies. The dithp nucleic acids are
XX additionally useful in somatic or germline gene therapy of the disorders
XX mentioned above, as a source of antisense sequences, as a source of
XX probes and primers, in genotyping and identification of individuals, in
XX the generation of transgenic animal models of human disease or knock in
XX humanised animals, in toxicological testing, and in transcript imaging.
XX The present sequence represents a dithp cDNA encoding a DITHP protein
XX which is an organelle-associated protein. Note: The sequence data for
XX this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 2213 BP; 422 A; 751 C; 633 G; 407 T; 0 U; 0 Other;

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## Alignment Scores:

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Pred. No.: 1.05e-156 Length: 2213
Score: 1418.00 Matches: 277
Percent Similarity: 96.22% Conservative: 3

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Best Local Similarity: 95.19% Mismatches: 5
Query Match: 91.90% Indels: 6
DB: 7 Gaps: 2

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US-09-811-094-33 (1-298) x ACC46652 (1-2213)

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DB 326 GCCAGCAAGCAGATCGCGCCGACAGAGTACAAGGCGCATCGTGACTGCAATGTCCGC 385
QY 61 ILeProIysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
DB 386 ATCCCAAGGAGCAGGGCGTGTCTCTTGGAGGGGCAAGCTTCCCAACGTCATTCGC 445
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 446 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAGCAGATCTTCCTG 505
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 506 GGGGGCGTGGACAAGCACACGAGTCTCTGAGGTACTTTTCGGGGCAACCTGGCTCCGC 565
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QY 161 LeuValIysIleThrIysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
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QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 746 GTCCAGGCGATCATCATCTACCGGGCGGCTACTTCGGCGTGTACGATACGCCAAGGCG 805
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
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QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
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QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
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GenCore version 5.1.6  
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Run on: August 17, 2004, 18:03:19 ; Search time 93 Seconds  
(without alignments)  
1778.230 Million cell updates/sec

Title: US-09-811-094-33

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Searched: 682709 seqs, 277475446 residues

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Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/ina/backfiles.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1543	100.0	1212	4	US-09-620-312D-687
3	1454	94.2	897	4	US-09-434-354-2
4	1412	91.5	1177	3	US-08-961-871-9
5	1409	91.3	1747	4	US-09-566-921-66
6	1405	91.1	1259	3	US-08-961-871-11
7	1385.5	89.8	894	4	US-09-434-354-1
8	429.5	27.8	389	4	US-09-621-976-810
9	404.5	26.2	383	4	US-09-621-976-608
10	368	23.8	416	4	US-09-621-976-610
11	330	21.4	565	4	US-09-833-381-204
12	311	20.2	1816	3	US-09-188-930-262

13	311	20.2	1816	4	US-09-312-283C-262	Sequence 262, Appl
14	299.5	19.4	2663	4	US-09-620-312D-283	Sequence 283, Appl
15	294	19.1	289	4	US-09-016-434-622	Sequence 622, Appl
16	286	18.5	936	4	US-09-743-847-1	Sequence 1, Appli
17	286	18.5	1674	4	US-09-482-273-26	Sequence 26, Appl
18	283.5	18.4	876	4	US-09-501-558-1	Sequence 1, Appli
19	280	18.1	1443	4	US-09-160-119-3	Sequence 3, Appli
20	280	18.1	2095	4	US-09-160-119-3	Sequence 1, Appli
21	274.5	17.8	1267	4	US-09-796-766-19	Sequence 19, Appli
22	265	17.2	1192	3	US-09-142-565-1	Sequence 1, Appli
23	265	17.2	1231	4	US-09-808-457-1	Sequence 1, Appli
24	265	17.2	1231	4	US-09-423-410-3	Sequence 1, Appli
25	257.5	16.7	930	4	US-10-001-051B-1	Sequence 1, Appli
26	250.5	16.2	1255	1	US-08-518-878B-38	Sequence 38, Appl
27	250.5	16.2	1255	1	US-08-294-522B-38	Sequence 38, Appl
28	250.5	16.2	1255	2	US-08-470-868A-38	Sequence 38, Appl
29	250.5	16.2	1596	2	US-08-807-861A-38	Sequence 38, Appl
30	250.5	16.2	1596	3	US-09-210-681-38	Sequence 38, Appl
31	250.5	16.2	1596	3	US-08-946-719A-38	Sequence 38, Appl
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33	250	16.2	1625	4	US-09-796-766-17	Sequence 17, Appl
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44	242	15.7	1506	4	US-09-796-766-9	Sequence 9, Appli
45	240.5	15.6	340	4	US-09-833-381-1770	Sequence 1770, Ap

#### ALIGNMENTS

##### RESULT 1

US-09-434-354-3  
; Sequence 3, Application US/09434354  
; Patent No. 6562563  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Anne N.  
; APPLICANT: Cleveenger, William  
; APPLICANT: Wiley, Sandra Eileen  
; APPLICANT: Andreyev, Alexander Y.  
; APPLICANT: Frigeri, Luciano G.  
; APPLICANT: Velicelebi, Gonul  
; APPLICANT: Davis, Robert E.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING  
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS  
; FILE REFERENCE: 660088.433  
; CURRENT APPLICATION NUMBER: US/09/434,354  
; CURRENT FILING DATE: 1999-11-03  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 897  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-434-354-3

Alignment Scores:  
Pred. No.: 8,73e-182 Length: 897  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 4 Gaps: 0  
US-09-811-094-33 (1-298) x US-09-434-354-3 (1-897)

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QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
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QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGCAAGCAGATCGCCGCGACAGCAGTACAAGGGCATCGTGGACTGCTGCTCCGC 180
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATCCCAAGGAGCGGCGTCTCTCTTGGAGGGGCAACCTTGCACACGTCATTCGC 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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Db 301 GGGGCGTGGAGCAAGCACACAGTCTTGGAGGTACTTTCGGGCAACCTTGGCTCCGC 360
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Db 361 GGTGCGCGCGCGACCTCTCTCTGCTGTGTACCGCTGGATTTTGCAGAACCGCG 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTGCAGCGGACGTGGAAAGTACAGGACAGCGCGAGTTCGAGGCTTGGAGACTGC 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
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QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
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QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysValIle 298
Db 841 GGATGCGGGGCGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
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## RESULT 2

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US-09-811-094-33 (1-298) x US-09-620-312D-687 (1-1212)
; Sequence 687, Application US/096203:12D
; Patent No. 659662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyen
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
```

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; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunging
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 659662el Nucleic Acids and
; FILE REFERENCE: 784CIP23
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 687
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(1027)
US-09-620-312D-687

Alignment Scores:
Pred. No.: 1,37e-181 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-620-312D-687 (1-1212)
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QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaA 20
Db 131 ATGACGGAAACAGGCGCATCTCTTCCCAAGACATCTTGGCCGAGGACATCGCCGCGCC 190
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 191 ATCTCCAGAGCGCGCTGGCTCCATCGAGCGGTCAAGCTGCTGCTGAGTCCAGCAC 250
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 251 GCCAGCAAGCAGATCGCCGCGACAGCAGTACAAGGGCATCGTGGACTGCTGCTCCGC 310
QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 311 ATCCCAAGGAGCGGCGTCTCTCTTGGAGGGGCAACCTTGCACACGTCATTCGC 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 371 TACTTCCCACTCAAGCCCTCACTTCCCTTCAAGGATTAAGTACAAGCAGATCTTCC 430
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 431 GGGGCGTGGAGCAAGCACACGATTTCTGAGGTTACTTTCGGGGCAACCTTGGCTCCGC 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 491 GGTGCGCGCGCGGACCTCTCTCTGCTGTGTACCGCTGGATTTTGCAGAACCGCG 550
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 551 CTGCAGCGGACGTGGAAAGTCAAGCAGACAGCGGCTTCCAGGCTTGGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
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APPLICATION NUMBER: US/08/961,871  
 FILING DATE: 31-OCT-1997  
 CLASSIFICATION: 800  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/030,017  
 FILING DATE: 01-NOV-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ferber, Donna M.  
 REGISTRATION NUMBER: 33,878  
 REFERENCE/DOCKET NUMBER: 78-96  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (303) 499-8080  
 TELEFAX: (303) 499-8089  
 INFORMATION FOR SEQ ID NO: 9:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1177 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Mus musculus  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 94...990  
 US-08-961-871-9

Alignment Scores:  
 Pred. No.: 2,3e-165 Length: 1177  
 Score: 1412.00 Matches: 264  
 Percent Similarity: 94.97% Conservative: 19  
 Best Local Similarity: 88.59% Mismatches: 15  
 Query Match: 91.51% Indels: 0  
 DB: 3 Gaps: 0

US-09-811-094-33 (1-298) x US-08-961-871-9 (1-1177)

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Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 94 ATGGGGGATCAGGCTTTGAGCTTTCTTAAGGACTTCTGCGAGTGCATCGCGGGCGCC 153
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 154 GTCTCCAGACCGCGTCCGCCATCGAGAGGTCAAACTGCTGCTGAGGTCCAGCAT 213
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 214 GCCAGCAACAGATCAGTGCAGAGAAGCAGTACAAAGGCATCATTTGATTCGTGTCGAGA 273
Qy 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyValAsnLeuAlaValIleArg 80
Db 274 ATCCCAAGAGCAGCGCTTCTCTCTTTCTGGAGGGTAACTGGCCACGATGATCCGG 333
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 334 TACTTCCCACTCAAGCCCTGAACCTTCGCTTCAAGACAGTACAGCAGATCTTCTCTG 393
Qy 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 394 GGAGGCGTGTATCGACATAAGCAGTCTTGGCGCTACTTCTGCTGAACCTGGGCTCTGGT 453
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 454 GGGGCGAGTGGGGCCACCTCCCTCTGCTTACCCGCTGGACITTCGTAGGACCCAGC 513
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 514 CTGGCTCGGACGCGGGCAAGGGATCTCCACGCGAGAATTCATGGGCTGGGCGACTGT 573
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 574 CTCACCAAGATCTTCAAGTCGGAGCGGCTCAAGGGTCTCTACAGGGTTTCAGTGTCTCT 633

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Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 634 GTCCAGGGCATCATCATCTACAGAGCTGCTTACTTCCGAGTCTATGACACATGCCAAGGG 693
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 694 ATGCTGCCAGACCCCAAGAAATGTGCACATATTCGTGAGCTGCATGATTCGCCAGAGTGTG 753
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValAlaCysArgMetMetMet 240
Db 754 ACAGCGTTGCGGGCTGGTGTCCTTATCCGTTTGACACTGTTTCGCGTAGGATGATGATG 813
Qy 241 GlnSerGlyArgGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 814 CAGTCTGGCCGCAAGAGGCTGATATTATGTACACGGGACACTTGTACTGCTGGAGGAAG 873
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 874 ATTGCAAAAGATGAAGAGGCCAACGCTTCTTCAAAGGTGCTTGTCTCAATGTACTGAGA 933
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db 934 GGCATGGGTGGTGGCTTTTGTATTGTTGATGATGATGATGATGATGATGATGATG 987

```

# RESULT 5

US-09-566-921-66  
 ; Sequence 66, Application US/09566921  
 ; Patent No. 6682888  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loring, Jeanne F.  
 ; APPLICANT: Tingley, Debra W.  
 ; APPLICANT: Edwards, Carla M.  
 ; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE  
 ; FILE REFERENCE: PA-0024 US  
 ; CURRENT APPLICATION NUMBER: US/09/566,921  
 ; CURRENT FILING DATE: 2000-05-05  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 66  
 ; LENGTH: 1747  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. 6682888 244561.6  
 US-09-566-921-66

Alignment Scores:  
 Pred. No.: 9,79e-165 Length: 1747  
 Score: 1409.00 Matches: 263  
 Percent Similarity: 94.63% Conservative: 19  
 Best Local Similarity: 88.28% Mismatches: 16  
 Query Match: 91.32% Indels: 0  
 DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-566-921-66 (1-1747)

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Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaAala 20
Db 126 ATGGGTGATCAGGCTTGGAGCTTCTTAAGGACTTCTTGGCGGGCGGCTGCGCGCTGCC 185
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 186 GTCTCCAGACCGCGTCCGCCATCGAGAGGTCAAACTGCTGCTGAGGTCCAGCAT 245
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 246 GCCAGCAACAGATCAGTGTGAGAGCAGTACAAAGGGATCATTGATTTGTGTGTGAGA 305
Qy 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyValAsnLeuAlaValIleArg 80
Db 306 ATCCCAAGAGCAGGGCTTCTCTCTTCTGGAGGGGTAACTGGCCAGATGATTCCT 365

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QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnPheLeu 100
DB 366 TACTTCCCAACCCAGCTCTCACTTCGCTTCAAGGACAGTACAGCAGCTCTTTA 425
QY 101 GlyGlyValAspLysHisThrGlnPheTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 426 GGGGTGTGGATGGGATCAAGCAGTTCTGGGGCTACTTTGTGTGTAACCTGGCGTCCGGT 485
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaThrArg 140
DB 486 GGGGCGGTGGGGCCACCTTCCTTTGCTTACCGCTGGACTTGTGTAGACAGG 545
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 546 TTGGCTGTGTATGGGCAAGGGCGCCCGCCAGCGTCAAGTTCCTGGCGCACTGT 605
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 606 ATCATCAAGATCTTCAAGTCTGATGGCTGAGGGGGCTCTACCAAGGGTTTCAAGCTCTCT 665
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 666 GTCCAAGGCATCATTTATATAGAGTGCCTACTTCGGAGTCTATGATCTGCAAGGG 725
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
DB 726 ATGCTGCTGATGCCCAAGAGCGCATATTTGTGAGCTGGATGATGGCCAGAGTGT 785
QY 221 ThrAlaValAlaGlyValSerTyrProPheAspThrValArgArgMetMetMet 240
DB 786 ACGCAGTTCGAGGGCTGTCTCTACCCCTTTCACACTGTTCGTGTAGATGATG 845
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
DB 846 CAGTCCGGCCGGAAGGGCGCATATTTATGATACACGGGACAGTGTGCTGGAGGAAG 905
QY 261 IlePheArgAspGluGlyGlyValAlaPheLysGlyAlaTyrSerAsnValLeuArg 280
DB 906 ATTGCAAGAGCAGAGGAGCCAGCCCTTCAAGAGTGTCTGATGATGATCAAAAAATATGTC 965
RESULT 6
US-08-961-871-11
; Sequence 11, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: MacGregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,871
; FILING DATE: 31-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
```

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; APPLICATION NUMBER: US 60/030,017
; FILING DATE: 01-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Feiber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 78-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1259 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 190..1086
; US-08-961-871-11
Alignment Scores:
Pred. No.: 1-87e-164 Length: 1259
Score: 1405.00 Matches: 263
Percent Similarity: 94.30% Conservative: 18
Best Local Similarity: 88.26% Mismatches: 17
Query Match: 91.06% Indels: 0
DB: 3 Gaps: 0
US-09-811-094-33 (1-298) x US-08-961-871-11 (1-1259)
QY 1 MetThrGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 190 ATGGGGATCAGCTTTTGAAGCTTCTTAAAGGACTTCTCTGGCAGGTGGCATCCCGCGCC 249
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 250 GTCTCCAAAGCGCGTCCCGCATCGAGAGGGTCAAACTGCTGCTGAGGTCAGCAT 309
QY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 310 GCCAGCAACAGATCAGTCAGAGAGAGAGTACAAAGGCATCATTTGTTGCTGTGAGA 369
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 370 ATCCCAAGAGCAGGGCTTCTCTCTTCTGGAGGGTAACTGGCCCAACGTGATCCGG 429
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 430 TACTTCCCACTCAAGCCCTGAACCTTCGCTTCAAGACAGTACAAAGCAGATCTTCCTG 489
QY 101 GlyGlyValAspLysHisThrGlnPheTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 490 GGAGGGGTGGATGCCATAAGCAGTTCTGGCGCTACTTTGCTGGTAACCTGGCTCTGT 549
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 550 GGGGAGCTGGGGCCACCTCCCTCTGCTCTACCCGCTGAGACTTGTGTAGGACAGG 609
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 610 CTGGCTGCCGCGTGGGCAAGGATCTTCCAGCAGAGATTCATATGGGCTGGCGCACTGT 669
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 670 CTCACCAAGATCTTCAAGTCGAGCGGCTGACGGGTCTCTACAGGGTTCTAGTGTCTCT 729
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 730 GTCCAGGGCATCATCATCTACAGAGCTGCTACTTCGGAGTCTATGACACTGCCAAGGG 789
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
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US-09-811-094-33 (1-298) x US-09-621-976-810 (1-389)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20  
Db 104 ATGACGGAACAGCCCATCTCTCGCCAAAGACTTCTTGGCCGGAS--ATCGCCGCGGCC 161  
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
Db 162 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGTCAGCTGCTGTCGAGTCCAGCAC 221  
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
Db 222 GCCAGCAAGCAGATCGCCCGCAGCAGTACAGGGCATCGTGGACTGCATTGTCGCG 281  
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80  
Db 282 ATCCCCAAGAGCAGCGCGTGTCTCTTCCTGAGGGGCAACCTTGCACCAACGTCATTGCG 341  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLys 92  
Db 342 TACTTCCGMACTCAAGCCCTCAACTTGGCTTCAAG 377

## RESULT 9

US-09-621-976-608  
; Sequence 608, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 608  
; LENGTH: 383  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 105...383

US-09-621-976-608  
Alignment Scores:  
Pred. No.: 3,51e-41 Length: 383  
Score: 404.50 Matches: 87  
Percent Similarity: 94.5% Conservative: 0  
Best Local Similarity: 94.5% Mismatches: 5  
Query Match: 26.22% Indels: 1  
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-621-976-608 (1-383)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20  
Db 105 ATGACGGAACAGCCCATCTCTTSCCAAAGACTTCTTGGCCGGAG--ATCGCCGCGGCC 162  
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
Db 163 ATCTCCAAAGCGCGCTGCTCGATCGAGCGGTCAGCTGCTGTCGAGTCCAGCAC 222  
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
Db 223 GCCAGCAAGCAGATCGCCCGCAGCAGTACAGGGCATCGTGGACTGCATTGTCGCG 282  
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80  
Db 283 ATCCCCAAGAGCAGCGCGTGTCTCTTCCTGAGGGGCAACCTTGCACCAACGTCATTGCG 342  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLys 92

Db 343 TACTTCCCACTCAAGCCCTCAASTTCCGCTTCAA 378

## RESULT 10

US-09-621-976-610  
; Sequence 610, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 610  
; LENGTH: 416  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 142...414  
; NAME/KEY: misc feature  
; LOCATION: 150,152,162,172  
; OTHER INFORMATION: n=a, g, c or t

US-09-621-976-610  
Alignment Scores:  
Pred. No.: 1.33e-36 Length: 416  
Score: 368.00 Matches: 74  
Percent Similarity: 95.18% Conservative: 5  
Best Local Similarity: 89.16% Mismatches: 4  
Query Match: 23.85% Indels: 1  
DB: 4 Gaps: 0

US-09-811-094-33 (1-298) x US-09-621-976-610 (1-416)

QY 116 AsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAsp 135  
Db 167 ATCTGTCATCGGTGGGCCGAGGCC--ACATCCCTGTGTTTGTACCTCTGTAT 225  
QY 136 PheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArg 155  
Db 226 TTTRCCGTACCCGCTCTAGCAGCTGATGGGTAAAGCTGGAGCTGAAGGGAATTCGA 285  
QY 156 GlyLeuGlyAspCysLeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGln 175  
Db 286 GGCTCGGTGACTGCTGTGTTAAGATCTACAAATCTGATGGGATTAAGGCGCTGTACCA 345  
QY 176 GlyPheSerValSerValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyr 195  
Db 346 GGCTTAAACATGTCTGTGAGGGTATTATCACTACCGAGCGCTCTTCGGTATCTAT 405  
QY 196 AspThrAla 198  
Db 406 GACACTGCA 414

## RESULT 11

US-09-833-381-204/c  
; Sequence 204, Application US/09833381  
; Patent No. 6672186  
; GENERAL INFORMATION:  
; APPLICANT: Robison, Keith E.  
; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs  
; FILE REFERENCE: 5800-119  
; CURRENT APPLICATION NUMBER: US/09/833,381  
; CURRENT FILING DATE: 2001-04-11  
; PRIOR FILING DATE: 09/516.448  
; NUMBER OF SEQ ID NOS: 2050  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 204

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; LENGTH: 565
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-204

Alignment Scores:
Pred. No.: 1.09e-31 Length: 565
Score: 330.00 Matches: 69
Percent Similarity: 76.72% Conservative: 20
Best Local Similarity: 59.48% Mismatches: 22
Query Match: 21.39% Indels: 5
DB: 4 Gaps: 1

US-09-811-094-33 (1-298) x US-09-833-381-204 (1-565)

QY 184 IleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGlyMetLeuPro 203
Db 565 ATCATGTGTACCGAGCCTCTATTTCGGAGCTTATGACAGTTATGACAGTTAAGGTTATTATACCA 506

QY 204 AspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThr--ValThrAlaV 223
Db 505 AAGCCACAGAAAACCCATTCTTGTCTCTCTTTTCATTTGCTCAAGTTGAGTACTACAT 446

QY 223 alAlaGlyValValSerTyrProPheAspThrValArgArgMetMetGlnSerG 243
Db 445 GCTCTGGAATACTTCTTCTATCCCTTTGACAGTTAGAACGCTATGATGACGAGTG 386

QY 243 lYArgLysGlyAlaAspIleMetTyrThrGlyThr-ValAspCysTrpArgLysIlePhe 262
Db 385 GTGAG-----GCTAAACGGCAATATAAAGAACCTTTAGACTGCTTTGTGAAGATATAC 332

QY 263 ArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArgGlyMet 282
Db 331 CAACATGAAGGAATCAGTTCCTTTTTCGTGGCGCCTTCTCCAAATGTTCTTCGCGGTACA 272

QY 283 GlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 271 GGGGTGCTTGTGTTGTATATATATATATATATAAATAAAGAA 230

RESULT 12
US-09-188-930-262
; Sequence 262, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188,930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-188-930-262

Alignment Scores:
Pred. No.: 1.43e-28 Length: 1816
Score: 311.00 Matches: 88
Percent Similarity: 50.17% Conservative: 62
Best Local Similarity: 29.43% Mismatches: 111
Query Match: 20.16% Indels: 38
DB: 3 Gaps: 11

US-09-811-094-33 (1-298) x US-09-188-930-262 (1-1816)

QY 10 LysAspPheLeuAlaGlyGlyIleAlaAlaIleSerLysThrAlaValaProfile 29

```

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Db 623 AGGCACCTGGTGGCAGGAGGTGGGCAGGGCAGTTTCCAGAACTGCTGACTGCCCTCTG 682
QY 30 GluArgValLysLeuLeuGlnValGlnHisAlaSerLysGlnIleAlaAlaAspLys 49
Db 683 GACAGACTGAAGTGTCTATGCAGGTC---CATGCTCCCGC-----AGC 724

QY 50 GlnTyrLysGlyIleValAspCysIleValArgIleProLysGluGlnGlyValLeuSer 69
Db 725 AACAAACATGTGTCATCTAGTGGATTACACAGATGATTTCGAGAGGGGGAGCCCAAGTCA 784

QY 70 PheTrpArgGlyAsnLeuAlaAsnValIleArgTyrPheProThrGlnAlaLeuAsnPhe 89
Db 785 CTCTGGCGGGCAACGGCATCATGTCTCTAAATGCTCCCTGAGTCGCCCAATATTC 844

QY 90 AlaPheLysAspLysTyrLysGlnIlePheLeuGlyValAspLysHisThrGlnPhe 109
Db 845 ATGGCATATGACAGATGAACGG-----CTTGTGGTAGTGTATCAGAGACG----- 892

QY 110 TrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGlyValaThrSerLeuCys 129
Db 893 ---CTGAGGATCCAGAAAGGCTTGTGGCAGGCTCCTTGGCGGAGCCATTGCCACAGT 949

QY 130 PheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGly 149
Db 950 AGCATCTACCCCAATGGAGTTCCTGAAGACCCGATGGCC-----CTGCGGAACAAGCA 1003

QY 150 ThrGluArgGluPheArgGlyLeuGlyAspCysLeuValLysIleThrLysSerAspGly 169
Db 1004 -----CAGTATCCGGCATCTGTCAGAGTGTGCCAGGAGGATCTTGGCTAAAGAGGT 1054

QY 170 IleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIleIleIleIleIleIle 189
Db 1055 GTAGTCCTCTTACAAAGGTACATCCCAACATGCTGGGATCATCCCTATGCTGCG 1114

QY 190 AlaTyrPheGlyValTyrAspThrAlaLysGlyMetLeuProAspProLysAsnThrHis 209
Db 1115 ATCGACCTAGCTGTCTATGAGACATTG-----ValValSerTrpMetIleAlaGln 1153

QY 210 Ile-----ValValSerTrpMetIleAlaGln 218
Db 1154 CTTCCAGCGTACGAGTAAACAGTGCAGACCCCGGTGTGTTGCTGCTCTGCGCTGTGT 1213

QY 219 ThrValThrAlaValAlaGly---ValValSerTyrProPheAspThrValArgArg 237
Db 1214 ACTATCTCCAGTACTTGTGGCCAGCTGGCCAGCTACCCACACTAGCCCTGTGTGAGGACCCGG 1273

QY 238 MetMetGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCys 257
Db 1274 ATGACGGCAACAGCTCCATTGAGGGCGCACCTGAGGTAAACCATGAGCAGCCCTC----- 1327

QY 258 TrpArgLysIlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsn 277
Db 1328 TTCAACACATCTCGGACTGAGGGGCTTTGGGCTCTACCGGGGCTGCGCCCAAC 1387

QY 278 ValLeuArgGlyMetGlyGlyAlaPheVal---LeuValLeuTyrAspGluLeuLys 295
Db 1388 TTCAATGAAGTGTATCCCGCTGTGAGCATCAGTGTGTCTACGAAACCTGAAG 1444

RESULT 13
US-09-312-283C-262
; Sequence 262, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2

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; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Mouse
US-09-312-283C-262

Alignment Scores:
Pred. No.:      1,43e-28      Length:      1816
Score:          311.00        Matches:     88
Percent Similarity: 50.17%    Conservative: 62
Best Local Similarity: 29.43% Mismatches:   111
Query Match:      20.16%     Indels:       38
DB:               4         Gaps:         11

US-09-811-094-33 (1-298) x US-09-312-283C-262 (1-1816)

QY 10 LysAspPheLeuAlaGlyGlyIleAlaAIAleSerLysThrAlaValAlaProIle 29
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QY 30 GluArgValLysLeuLeuGlnValGlnHisAlaSerLysGlnIleAlaAAspiLys 49
Db 683 GACAGACTGAAGTGCTCATGCAGATC-----CATGCTCCGC-----AGC 724
QY 50 GlnTyrlsGlylileValaspCyislleValarglleProLysGluGlnGlyValLeuSer 69
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QY 70 PheTrpArgGlyAsnLeuAlaAsnValIleArgTyrlPheProThrGlnAlaLeuAsnPhe 89
Db 785 CTCTGGCGGGCACCGCATCATGTCTCTCAAATGCCCCGTGAGTCGCCCATCAATTC 844
QY 90 AlaPheLysAspLysTyrlsGlnIlePheLeuGlyValasPlsHisThrGlnPhe 109
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Db 893 ---CTGAGNATCCAGAAAGCGTTGTGGCAGGCTCTTGGCCGGAGCCATTCGCCAGAGT 949
QY 130 PheValtyrProLeuAspPheAlaArthrArgLeuAlaAlaAspValGlyLysSerdly 149
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QY 150 ThrGluArgGluPheArgGlyLeuGlyAspCysLeuValLysilleThrLysSerAspGly 169
Db 1004 -----CAGTACTCCCGCATCGTGGACTGTGCCAGGAGCATCTTGGCTAAAGAGGGT 1054
QY 170 IleArgGlyLeuTyrlGlnGlyPheSerValserValGlnGlyIleIleIleTyrlArgAla 189
Db 1055 GTAGTCGCTTCTACAAGAGCTACATCCCACACATGCTGGGATCATCTCCATGTCTGGC 1114
QY 190 AlaTyrlPheGlyValTyrlAspThrAlaLysGlyMetLeuProAspProllysAsnThrHis 209
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QY 210 Ile-----ValValserTrpMetIleAlaGln 218
Db 1154 CTCAGCGCTACCCAGTAACAGTCGACAGACCCCGGTGTGTCCTCTCGCTCTGTGGT 1213
QY 219 ThrValThrAlaValAlaGly---ValValserTyrlProPheAspThrValArgArg 237
Db 1214 ACTATCTCCAGTACTTGTGGCCAGCTGGCCAGCTACCCCACTAGCCCTGGTCAGGACCCGG 1273
QY 238 MetMetMetClnSerGlyArgLysGlyAlaAspIleMetTyrlThrValAspCys 257
Db 1274 ATCAGGCAACAGCCCTCCATGTGGGCGCGCCTCGAGGTAAACATGAGCAGCTC----- 1327
QY 258 TrpArgLysIlePheArgAspGluGlyValLysAlaPheLeuGlyValatirPheSerAsn 277

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Db 1264 TATGAGGGCTTCTTTGGACTCTACAGGGTCTGTATACCAACATTATAGGGTGTCTCCA 1323  
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Db 1324 GAAAGGCGCAATAACTGACTGTTAATGATTTTTCGGGCAAAATTTACCAAGAGAT 1383  
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
Db 1384 GGCTCTGTTCCTCA-----CTTCCAGCAGAAATTTCTGTGGA 1419  
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
Db 1420 GGCTGTCTGGAGGCTCTCAGGTCATTTTACCAACCATTTGGAGTAGTGAAGATTCGT 1479  
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
Db 1480 CTGCAAGTA---GCTGGAGAGATCACCACGGGACCCAGAGTCAGCGCCCTG----- 1527  
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
Db 1528 -----AATGTGCTCCGGGACTTGGGAATTTTGTCTGTATAGGTCGCAAGCGGT 1581  
QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
Db 1582 TTCCTCCGAGACATTCCTCTCTGCAATCTATTTTCTGTATTATGCTCATTCGAACTA 1641  
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
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QY 221 ThrAlaValAlaGlyVal-----ValSerTyrProPheAspThrValArgArg 236  
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QY 237 ArgMetMetGlnSerGlyArgGlyAlaAspIleMetTyrThrGlyThrValAsp 256  
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QY 257 CysTrpArgLysIlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSer 276  
Db 1807 TGTTCAGGAAGATTCTCCGGGAAGAGAGGGCCCTCAGCATTTTGGAAAGGAGCTGCAGCT 1866  
QY 277 AsnValLeuArgGlyMetGlyGly---AlaPheValLeuValLeuTyrAspGluLeuLys 295  
Db 1867 CGAGTGTTCGATCCTCTCCCGAGTTGGTGTGTTACCTTGTCTCACTTATGAAGTCTCCAG 1926  
QY 296 Lys 296  
Db 1927 CGG 1929

## RESULT 15

US-09-016-434-622  
; Sequence 622, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 622:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 289 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: LIVRUT04  
; CLONE: 2517151  
US-09-016-434-622  
Alignment Scores:  
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Score: 294.00 Matches: 65  
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Query Match: 19.05% Indels: 1  
DB: 4 Gaps: 0  
US-09-811-094-33 (1-298) x US-09-016-434-622 (1-289)  
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QY 21 IleSerLysThrAlaValAlaAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
Db 153 ATCTCCAAAGACGGCGGTGCTCCGATCCGAGCGGGTCAAGCTGCTGCTCAGGTCCAGCAC 212  
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
Db 213 GCCAGCAAGCAGATCGCCGCCGACAGCAGTACAAAGGCGCATCGTGGACTGCAT-GTCCGC 271  
QY 61 IleProLysGluGlnGly 66  
Db 272 ATCCCCAAGGAGCAGGGC 289

Search completed: August 17, 2004, 20:25:07  
Job time : 133 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 17, 2004, 19:33:59 ; Search time 530 Seconds  
(without alignments)

2758.810 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543

Sequence: 1 MTEQAISPAKQFLAGGIAAA.....LRMGGAFFVLYDELKKVI 298

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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:

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19: /cg2\_6/ptodata/2/pubna/US6\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	1543	100.0	897	9	US-09-810-644-3	Sequence 3, Appli
3	1543	100.0	897	9	US-09-185-904A-3	Sequence 3, Appli
4	1543	100.0	1212	15	US-10-037-270-687	Sequence 687, App
5	1543	100.0	1212	16	US-10-117-722-687	Sequence 687, App
6	1510	97.9	2592	14	US-10-044-090-152	Sequence 152, App
7	1463	94.8	1385	16	US-10-062-674-1973	Sequence 1973, Ap
8	1454	94.2	897	9	US-09-811-094-2	Sequence 2, Appli
9	1454	94.2	897	9	US-09-810-644-2	Sequence 2, Appli
10	1454	94.2	897	9	US-09-185-904A-2	Sequence 2, Appli
11	1454	94.2	1228	16	US-10-116-275-301	Sequence 301, App
12	1451	94.0	1215	16	US-10-191-803-135	Sequence 135, App
13	1446	93.7	1243	13	US-10-403-571-153	Sequence 153, App
14	1424	92.3	1196	9	US-09-917-800A-1327	Sequence 1327, Ap
15	1409	91.3	1711	15	US-10-198-846-13437	Sequence 13437, A
16	1385.5	89.8	894	9	US-09-811-094-1	Sequence 1, Appli
17	1385.5	89.8	894	9	US-09-810-644-1	Sequence 1, Appli
18	1385.5	89.8	894	9	US-09-185-904A-1	Sequence 1, Appli
19	1385.5	89.8	1320	10	US-09-738-630-70	Sequence 70, Appl
20	1356.5	87.9	1116	9	US-09-969-708-213	Sequence 213, App
21	1356.5	87.9	1116	9	US-09-880-107-2096	Sequence 2096, Ap
22	1356.5	87.9	1116	15	US-10-171-581-48	Sequence 48, Appl
23	1193	77.3	2706	15	US-10-103-313-611	Sequence 611, App
24	1193	77.3	2706	16	US-10-158-034-121	Sequence 121, App
25	1184.5	76.8	925	16	US-10-161-927-5	Sequence 5, Appli
26	1081	70.1	687	16	US-10-264-049-2162	Sequence 2162, Ap
27	1021.5	66.2	977	16	US-10-369-493-29759	Sequence 29759, A
28	1003	65.0	976	16	US-10-369-493-29790	Sequence 29790, A
29	993.5	64.4	903	16	US-10-369-493-28775	Sequence 28775, A
30	979.5	63.5	5768	10	US-09-873-167C-134	Sequence 134, App
31	936	60.7	720	9	US-09-910-943-105	Sequence 105, Appl
32	840	54.4	639	17	US-10-404-460-10	Sequence 10, Appl
33	811	52.6	537	13	US-10-029-386-20882	Sequence 20882, A
34	809.5	52.5	612	13	US-10-424-599-50040	Sequence 50040, A
35	796	51.6	943	12	US-09-876-143-1254	Sequence 1254, Ap
36	793.5	51.4	543	13	US-10-621-901-2291	Sequence 2291, Ap
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44	751.5	48.7	1593	13	US-10-424-599-25174	Sequence 25174, A
45	751	48.7	1523	13	US-10-425-114-26646	Sequence 26646, A

# ALIGNMENTS

## RESULT 1

US-09-811-094-33  
; Sequence 3, Application US/09811094  
; Patent No. US20010044144A1

; GENERAL INFORMATION:  
; APPLICANT: Anderson, Christen M.

; APPLICANT: Davis, Robert E.  
; APPLICANT: Clevenger, William

; APPLICANT: Wiley, Sandra Bileen  
; APPLICANT: Willer, Scott W.

; APPLICANT: Szabo, Tomas R.  
; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Moos, Walter H.  
; APPLICANT: Pei, Yazhong

; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
; FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR  
; CURRENT APPLICATION NUMBER: US/09/811,094  
; CURRENT FILING DATE: 2001-03-14

; NUMBER OF SEQ ID NOS: 37  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 3  
; LENGTH: 897

TYPE: DNA  
ORGANISM: Homo sapien  
US-09-811-094-3

Alignment Scores:  
Pred. No.: 1.67e-202 Length: 897  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-811-094-3 (1-897)

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QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 121 GCCAGCAAGCAGATCGCCGCCGACAGCAGTACAAGGGCATCGTGGACTGCTTCCGC 180
QY 61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyAsnLeuAlaAsnValIleArg 80
DB 181 ATCTCCAAAGAGGAGCGGCTGTCTCTTCTTGGAGGGGCAACCTTGCCAAAGCTATTCCG 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 301 GGGGGCGTGGACAGCAGCAGTCTTGGAGGTACTTGGGGGCAACCTTGCCCTCCGGC 360
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 421 CTGGCAGCGGAGCTGGGAAAGTACAGCAGCAGCGCGAGTCTCCAGGCTCGGAGACTGC 480
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# RESULT 2

US-09-810-644-3

Sequence 3, Application US/09810644  
Patent No. US20020012992A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, Christen M.  
APPLICANT: Davis, Robert E.  
APPLICANT: Clevenger, William  
APPLICANT: Wiley, Sandra Eileen  
APPLICANT: Willer, Scott W.  
APPLICANT: Szabo, Tomas R.  
APPLICANT: Ghosh, Soumitra S.  
APPLICANT: Moos, Walter H.  
APPLICANT: Fei, Yazhong  
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),  
FILE REFERENCE: 660088.420D3  
CURRENT APPLICATION NUMBER: US/09/810,644  
CURRENT FILING DATE: 2001-03-14  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 3  
LENGTH: 897  
TYPE: DNA  
ORGANISM: Homo sapien  
US-09-810-644-3

Alignment Scores:  
Pred. No.: 1.67e-202 Length: 897  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-810-644-3 (1-897)

```

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 1 ATGACGGAACAGCCATCTCTTGGCCAAAGACTTCTTGGCCGAGGATCGCCGCCGCC 60
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 61 ATCTCCAAAGACGGCGTGGCTCCGATCGAGCGGTCAAGCTGCTGCTGACGATCCAGC 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 121 GCCAGCAAGCAGATCGCCGCCGACAGCAGTACAAGGGCATCGTGGATGCTGATTCGCG 180
QY 61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyAsnLeuAlaAsnValIleArg 80
DB 181 ATCTCCAAAGAGGAGCGGCTGTCTCTTCTTGGAGGGGCAACCTTGCCAAAGCTATTCCG 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 241 TACTTCCCACATCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAGCAGATCTTCTCG 300
QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 301 GGGGGCGTGGACAGCAGCAGTCTTGGAGGTACTTGGGGGCAACCTTGCCCTCCGGC 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGTGGCGGGCGGCGGACCTCCCTCTGCTGTATCCCGCTCGATTTTGCAGAACCCGCG 420
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 421 CTGGCAGCGGAGCTGGGAAAGTACAGCAGCAGCGGAGTTCGAGGCTCGGAGACTGC 480
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 481 CTGGTGAAGATCACCAGTCCGACGGCATCCGGGGCTGTACACAGGCTTCAAGTGTCTCC 540

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Qy	61	IleProIysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
Db	181	ATCCCAAGAGCAGGGCGTGCTGCTTCCTCGAGGGCAACCTTGGCAACGTCAATTCGC	240
Qy	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
Db	241	TACTTCCCACCTCAAGCCCTCAACTTCGCCTTCAAGGATAGTACAGCAGATCTTCTGT	300
Qy	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
Db	301	GGGGCGGTGGCAAGCACACGAGATTCTGGAGGTACTTTGCGGCACACCTGGGCTCCGGC	360
Qy	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg	140
Db	361	GGTGGCGCGGGCGGCACTCCCTCTGCTTCGTGTACCGCTGGATTTTGCAGAACCCGC	420
Qy	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
Db	421	CTGGCAGCGGACGTGGGAAAGTCAAGGCACAGCGCGAGTTCCGAGGCCCTGGGAGACTGC	480
Qy	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer	180
Db	481	CTGGTGAAGATCCCAAGTCCGACGGCATCCGGGCGCTTACCAGGGCTTCAGTGTCCTC	540
Qy	181	ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly	200
Db	541	GTGCAAGGCATCATCTATCCGGCGCGCCCTACTTCGCGGTGTACGATACGGCCCAAGGC	600
Qy	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
Db	601	ATGCTCCCCGACCCCAAGAACACGCACATCGTGTGTAGCTGGATGATCGCGCAGACCGTG	660
Qy	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgGmetMetMet	240
Db	661	ACGGCGGTGGCGGGGTGTGTGTCCTACCCCTTCGACACGGTGGCGGCGCATGATGATG	720
Qy	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
Db	721	CAGTCCGGCGCGAAAGAGCTTGACATCATGTGTACACGGCACCGTCGACTCTTCGAGGAAG	780
Qy	261	IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyValaTrpSerAsnValLeuArg	280
Db	781	ATCTTCAGAGATAGGGGGGGCAAGCCCTTCTTCAGGGGTGCTGTGTTCCACAGTCTCTGGCG	840
Qy	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle	298
Db	841	GGCATGGGGGGCGCCCTCGTCTGCTGCTGTACACGAGCTCAAGAAGGTGATC	894

US-09-185-904A-3

```

0036-5577-2780-081
> Publication No. US20030104529A1
> GENERAL INFORMATION:
> APPLICANT: Tang, Y. Tom
> APPLICANT: Liu, Chenghua
> APPLICANT: Asundi, Vinod
> APPLICANT: Zhang, Jie
> APPLICANT: Ren, Feiyang
> APPLICANT: Chen, Rui-hong
> APPLICANT: Zhao, Qing A.
> APPLICANT: Wehrman, Tom
> APPLICANT: Xue, Aidong J.
> APPLICANT: Yang, Yonghong
> APPLICANT: Wang, Jian-Rui
> APPLICANT: Zhou, Ping
> APPLICANT: Ma, Yundong
> APPLICANT: Wang, Dunrui
> APPLICANT: Wang, Zhiwei
> APPLICANT: Tillinghast, John
> APPLICANT: Drmanac, Radcoje I.
> TITLE OF INVENTION: No. US20030104529
> TITLE OF INVENTION: Polypeptides
> FILE REFERENCE: 784CIP2B

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QY	1	MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla	20
DB	1	ATGACGGAACAGGCCATCTCCCTCGCCAAAGACTTCTTGCCGAGGAGCATCGCCGCGCC	60
QY	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
DB	61	ATCTCAAGACGCGCGTGCTCCGATCGAGCGGTCAAAGTGTGCTSCAGGTCACAGCAC	120
QY	41	AlaSerLysGlnIleAlaAlaAspLysGlnThrLysGlyIleValAspCysIleValArg	60
DB	121	GCAGCAACAGCATCGCCCGCCAGCAGATCAAGGGCATCGTGGATCGATGTCTCGC	180



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Db      371  TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAGCAGATCTTCTG 430
Qy      101  GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db      431  GGGGCGTGGGAAAGACACACACAGTTCCTGGAGGTACTTTGGGGCAACCTGGCCCTCGGC 490
Qy      121  GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAatgThrArg 140
Db      491  GGTGGGCGGGCGGACCTCTCTCTGCTTCTGTTACCGCTGGATTTCGCCAGAACCCGC 550
Qy      141  LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db      551  CTGGCAGCGGACGTGGGAAGTCAAGGCACAGAGCGCAGATTCCGAGGCGCTGGGAGACTGC 610
Qy      161  LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db      611  CTGTGAAGATCACCAAGTCCGACCGCATCCGGGCGCTGTACCGAGGCTTCAGTGTCTCC 670
Qy      181  ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db      671  GTGCAGGCGCATCATCTACCGGGCGCTTCTTGGCGTGTACGATACGGCCAAGGCG 730
Qy      201  MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db      731  ATGCTCCCGACCCCAAGAACACACACATCTGTTGAGTGTGATCGGCGACACCGTG 790
Qy      221  ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db      791  ACGGCGTGGCGGGTGTCTTACCCCTTCACACCGTTCGCGCGCGCATGTATG 850
Qy      241  GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db      851  CAGTCCGGCGCAAGAGAGTGCATCATGTATACACGGCACCGTCTGTGGAGAAAG 910
Qy      261  IlePheArgAspGluGlyGlyValIleAlaPhePheLysGlyAlaTrpSerAsnValIleArg 280
Db      911  ATCTTCAGATGAGGGGGGAGGCGCTTCTCAAGGTGCTGTGTCACGCTCAAGAGGTGATC 970
Qy      281  GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db      971  GGCATGGGGGCGCTTCTGCTGCTGCTGTACGACGAGCTCAAGAGGTGATC 1024

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## RESULT 6

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US-10-044-090-152
; Sequence 152, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
; APPLICANT: Olga Bandman
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
; CURRENT APPLICATION NUMBER: US/10/044,090
; CURRENT FILING DATE: 2002-01-09
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: PERL Program
; SEQ ID NO 152
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
; NAME/KEY: unsure
; LOCATION: 1131, 1929
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-152

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Alignment Scores:
Pred. No.: 3 09e-197 Length: 2592
Score: 1510.00 Matches: 296
Percent Similarity: 99.33% Conservative: 2
Best Local Similarity: 99.67% Mismatches: 0
Query Match: 97.86% Indels: 2

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Db      14      Gaps: 0
US-09-811-094-33 (1-298) x US-10-044-090-152 (1-2592)
Qy      1  MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIle-AlaAlaAl 20
Db      207  ATGACGGAAACAGGCCATCTCTTCGCCAAAGACTTCTTTGGCGGGAGGCAATGGCCGCCGC 266
Qy      20  aIleSerLysThrAlaValAlaProIleGluArg-ValLysLeuLeuLeuValGlnH 40
Db      267  CATCTCCAGACGGCGCTGGCTCCGATCAGCGGGGTCAAGCTGCTGCTGCGAGGTCCAG 326
Qy      40  iSaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValAla 60
Db      327  ACGCCAGCAAGCAGATCGCGCGCCGCAAGCGCATCAAGGGCATCGTGGACTGCATTGTCC 386
Qy      60  rGileProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleAla 80
Db      387  GCATCCCCAAGAGCAGGCGCTGTCTCTTGGAGGGGCAACCTTGGCAACGTATTC 446
Qy      80  rGtyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheL 100
Db      447  GCTACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAGCAGATCTTCC 506
Qy      100  euGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerG 120
Db      507  TGGGGGCGCTGGACAAGCACACGCGATCTCTGAGGTACTTTGCGGCAACCTGGCCCTCG 566
Qy      120  lyGlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaAatgThrA 140
Db      567  GCGTGGCGGGCGGCGCACTCTCTGCTGTGTACCCGCTGGATTTTGCAGNACC 626
Qy      140  rGleuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspC 160
Db      627  GCCTGGCAGCGGACGTGGGAAAGTACAGGCACAGAGCGGAGTTCGAGGCTTGGGAGACT 686
Qy      160  yLeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValS 180
Db      687  GCTGTGTGAAGATCACCAAGTCCGCGGCATCCGGGGCTGTACAGGCTTCAGTGTCT 746
Qy      180  erValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysG 200
Db      747  CCGTGCAGGGCATCATCTACCGGGCGCTTCTGCGCTGTACGATACGGCCAAGG 806
Qy      200  lyMetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrV 220
Db      807  GCATGTCTCCCGACCCCAAGAACACACACATCTGTTGAGTGTGATGATCGCGCAGACCG 866
Qy      220  alThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetM 240
Db      867  TGAAGCGCTGGCGGCGGTGGTGTCTTACCCCTTCGACACCGTTCGCGCGCGCATGATGA 926
Qy      240  etGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgL 260
Db      927  TGCAGTCCGGCGCAAGAGGCTGACATCATGTACACGGGCAACCGTCTGCTGTGGAGGA 986
Qy      260  yIlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTrpSerAsnValIleAla 280
Db      987  AGATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGTGCGTGGTCCACGCTCTGC 1046
Qy      280  rGlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298
Db      1047  GGGGCATGGGGGCGCTTCTGCTGCTGTACGACGAGCTCAAGAGGTGATC 1102

```

## RESULT 7

```

US-10-062-674-1973
; Sequence 1973, Application US/10062674
; Publication No. US2004005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: FA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674

```

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; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 1973
; LENGTH: 1385
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 373719.5
US-10-062-674-1973

Alignment Scores:
Pred. No.: 3,61e-191 Length: 1385
Score: 1463.00 Matches: 275
Percent Similarity: 97.30% Conservative: 13
Best Local Similarity: 92.91% Mismatches: 8
Query Match: 94.82% Indels: 0
DB: 16 Gaps: 0

US-09-811-094-33 (1-298) x US-10-062-674-1973 (1-1385)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaA 20
Db 116 ATGACAGATGCGGTGTGCTTCCCAAGGACTTCTGGCAGGTGGAGTGGCGGAGCC 175
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 176 ATCTCCAGAGCGGGTAGGCCCATCGAGCGGTCAAGCTGCTGCTGCAGGTGCAGCAT 235
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAlaSerGly 60
Db 236 GCCAGCAAGCAGATCACTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT 295
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 296 ATTCCTCAAGGAGCGGAGGAGTCTCTCTCTGCGCGGTAACTGGCCCAATGTCATCAGA 355
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
Db 356 TACTTCCCAAGGAGGAGTCTTAACTTCCCTTCAAGATTAATACAGAGCATCTTCTCTG 415
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 416 GGTGGTGTGCACAGAGAACCCAGTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGGT 475
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 476 GGTGCCAGGAGGAGGAGCATCTCTGTGTTTGTGTACCTCTTGAATTTGGCCCATCCCGT 535
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 536 CTAGCAGCTGATGTGGGTAAAGCTGAGCTGAAAGGGAATTCAGGCGCTCGGTGACTGC 595
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 596 CTGTTTAAGATCTACAATCTGATGGGATTAAGGCGCTGTACCAAGGCTTTACGTTGTCT 655
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 656 GTGCAGGATATTATCATCTACCGAGCGGCTACTTCCGTATCTATGACATGTCAGAGGGA 715
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 716 ATGCTTCCGATCCCAAGAACCTCACTACATGCTGAGTGGATGATCGCACAGACTGTC 775
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 776 ACTGCTGTGGCGGTGACTTCTATCTATCTTACACCGGTTGCGCGCGCATGATGATG 835
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 836 CAGTCAGGGCGCAAGGAACTGACATCATGTACACAGGACGCTGCTGCTGGCGGAG 895
Qy 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyIleAlaTrpSerAsnValLeuArg 280
Db 896 ATTGCTGCTGATGAAGAGGCAAGGCTTTTTCAGGGTGCATGCTCAATGTTCTCAGA 955
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 956 GGCATGGGTGGTGGCTTTTGTCTGCTGTATGATGAATCAAGAG 1003

RESULT 8
US-09-811-094-2
; Sequence 2, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willer, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yehong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-811-094-2

Alignment Scores:
Pred. No.: 3,22e-190 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-811-094-2 (1-897)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaA 20
Db 1 ATGACAGATGCGGATGCTCTTCCCAAGGACTTCTGGCAGGTGGAGTGGCGGAGCC 60
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGCGGGTAGGCCCATCGAGCGGTCAAGCTGCTGCTGAGGTGCAGCAT 120
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60
Db 121 GCCAGCAAGCAGATCACTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT 180
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATTCAGAGGAGCAGGAGGATTTCTCTCTTGGCGCGTAACCTGGCCCAATGTCATCAGA 240
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
Db 241 TACTTCCCAAGGAGGAGGATTTTAACTTCCCTTCAAGATTAATACAGAGCATCTTCTCTG 300
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGGTGTGCACAGAGAGAACCCAGTTTGGCGCTACTTTTCAGGGAATCTGGCATCGGT 360
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
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Db 361 GGTGGCGAGGGGCGACATCCCTGTGTTTGTGTACCCCTTGTGATTTGGCCGCTACCCGT 420
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGCAGCTGATGTGGTAAAGCTGGAGCTGAAGAGGAATTCGAGGCTCGTGACTGC 480
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGGTTAAGATCTCAAAATCTCATGGGATTAGGGCCCTGTACCAAGGCTTTAAAGCTGTCT 540
Qy 181 ValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 541 GTGCAAGGTATTATCATCTACCGAGCGCCCTACTTCGGTACTATGACACTGCAAGGGA 600
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTTCGGGATCCCAAGAACTACATCGTCACTCAGCTGATGATCGCACAGACTGTC 660
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 661 ACTGCTGTGCGGGTGTGACTTCCTATTCATTTGACCGTTTCGCGCGCATGATGATG 720
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 721 CAGTCAGGCGGCAAGAGAACTGACATCATGTACACAGGCACGCTTGACTGCTGGCGAAG 780
Qy 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 781 ATTGCTGTGTGATGAAGAGGAAAGCTTTTTCAGAGGTGATGTCATGTCATGTTCTCAGA 840
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 841 GGCATGGTGGTGGCTTTTGTGCTTGTGTATGATGAATCAAGAAAG 888
```

## RESULT 9

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US-09-810-644-2
; Sequence 2, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pei, Yizhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-644-2
```

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Alignment Scores:
Pred. No.: 3,228-130 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Db: 9 Gaps: 0
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US-09-811-094-33 (1-298) x US-09-810-644-2 (1-897)

Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20

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Db 1 ATGACAGATCCGCTATGCTCTTCGCCAAGGACTTCTGCGAGTGTGAGTGGCGGAGCC 60
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGCGGGTAGCGCCATCGAGCGGGTCAAGCTGTCTGCTCAGGTGCGAGCAT 120
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCCAAGCAGAGATCATCTGCAGATAAGCAATACAAAGGCATTATAGACTGCGTGGTCCGT 180
Qy 61 IleProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 181 ATTCCCAAGAGCAGAGTTCCTCTCTGCGCGGTAACTGCGCCCAATGTCATCAGA 240
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCAACCCAGGCTCTTAACCTTCGCCTTCAAAGATAAATACAAAGCAGATCTTCTCTG 300
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGGTGTGGACAAAGAAACCCAGTTTTCGCGCTACTTTGCAGGGAATCTGGCATCGGT 360
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGTGGCGCAGGGGCCACATCCCTGTGTTGTGTACCTCTTGATTTTGCCCGTACCCGT 420
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGCAGCTGATGTGGGTAAAGCTGGAGCTGAAAGGGAATTCGAGGCGCTCGGTGACTGC 480
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 481 CTGGTTAAGATCTCAAAATCTGATGGGNTAAGGGCTGTACCAAGGCTTTTACGTTCT 540
Qy 181 ValGlnGlyIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 541 GTGCAAGGTATTATCATCTACCGAGCGGCTACTTCGGTATCTATGACACTGCAAGGGA 600
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTTCGGGATCCCAAGAACTACATCGTCACTCAGCTGATGATGATGATGATG 660
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 661 ACTGCTGTGCGGGTGTGACTTCCTATTCATTTGACCGCTTCGCGCGCATGATGATG 720
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 721 CAGTCAGGCGGCAAGGAACTGACATCATGTACACAGGCACGCTTGACTGCTGGCGAAG 780
Qy 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db 781 ATTGCTGTGTGATGAAGAGGCAAGCTTTTTCAGGGTGCATGTTCTCAATGTTCTCAGA 840
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
Db 841 GGCATGGTGGTGGCTTTTGTGCTTGTGTATGATGAATCAAGAAAG 888
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## RESULT 10

```
US-09-185-904A-2
; Sequence 2, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
```



490 CTAGCAGCTGATGTGGTAAAGCTGGAGCTGAAAGGAATTCGAGGCTCGGTGACTGC 549  
161 LeuVallyslleThrLysSerAspGlyleArgGlyLeuTyrGlnGlyPheSerValSer 180  
550 CTGGTTAAGATCTACAAATCTGATGGGATTAAAGGCTGTATACCAAGGCTTTTAAAGCTGTCT 609  
181 ValGlnGlylleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
610 GTGCAGGCTATTATCATCTACCGAGCGCTTACITCGTATCTATGACACTGCAAGGGA 669  
201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
670 ATGCTTCGGGATCCCAAGAACACTCACATCGTCATCGCTGATGATCGCACAGCTGTC 729  
221 ThrAlaValAlaGlyValIleValSerTyrProPheAspThrValArgAtgMetMetMet 240  
730 ACTGCTGTGTGGCTTGAATCTTCTATCCATTTGACACCGTTGCGCGCGCATGATGATG 789  
241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
790 CAGTCAGGCGGCAAGGAAGCACTGACATCATGTACACAGGCGGCTTGAAGTGGCGGAAG 849  
261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTyrSerAsnValIleArg 280  
850 ATGCTGTGTGATGAAGAGGAGGCAAGCTTTTTCAGGGTGTGATGTCATGTTCTCTAGA 909  
281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
910 GCATGGGTGGTCTTTGTGCTCTCTGTATGATGAATCAAGAAAG 957

RESULT 12

US-10-191-803-1135  
; Sequence 1135, Application US/10191803  
; Publication No. US20040014040A1  
; GENERAL INFORMATION:  
; APPLICANT: MENDRICK, Donna  
; APPLICANT: PORTER, Mark  
; APPLICANT: JOHNSON, Kory  
; APPLICANT: HIGGS, Brandon  
; APPLICANT: CASTLE, Arthur  
; APPLICANT: ELASHOFF, Michael  
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling  
; FILE REFERENCE: 4921-5090US  
; CURRENT APPLICATION NUMBER: US/10/191,803  
; CURRENT FILING DATE: 2002-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,819  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/305,623  
; PRIOR FILING DATE: 2001-07-17  
; PRIOR APPLICATION NUMBER: US 60/369,351  
; PRIOR FILING DATE: 2002-04-03  
; PRIOR APPLICATION NUMBER: US 60/377,611  
; PRIOR FILING DATE: 2002-05-06  
; NUMBER OF SEQ ID NOS: 1140  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1135  
; LENGTH: 1215  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 D12771  
US-10-191-803-1135

Alignment Scores:  
Pred. No.: 1,348-189 Length: 1215  
Score: 1451.00 Matches: 272  
Percent Similarity: 96.9% Conservative: 15  
Best Local Similarity: 91.8% Mismatches: 9  
Query Match: 94.0% Indels: 0  
DB: 15 Gaps: 0

US-09-811-094-33 (1-298) x US-10-191-803-1135 (1-1215)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20  
Db 55 ATACAGATGTCGCTGTGTCCTTCGCCAAGGACTTCTTGGCTGGTGGAGTGGCGGGCC 114  
QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnValGlnHis 40  
Db 115 ATCTCCAAGACGGCGGTAGCACCCATCGAGCGGGTCAAGCTGCTGCTGAGGTGCAGCAC 174  
QY 41 AlaserLysGlnIleAlaAlaLysGlnTyrLysGlyIleValAspCysIleValArg 60  
Db 175 GCCAGCAGCAATACCGGAGATTAAGCAATACAGGGCATATAGACTGCGGTGGTTCGT 234  
QY 61 IleProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80  
Db 235 ATCCCAAGGAACAGGAGTCTCTCTGCGGTGGCAACCTGGCCCAATGTCTATCAGA 294  
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
Db 295 TACTTCCCAACCCAGGCTCTCAACTTTCCTTCAAAGATAAATACAGGAGATCTTTTG 354  
QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
Db 355 GGTGGTGTGGACAAGAGGACCCAGTTTGGCGGTACTTTGCAGGGAACCTGGCATCAGGT 414  
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
Db 415 GGTGCTGCTGGGGCCACATCTTGTCTTTGTGTACCTCTTGAATTTGCCCGTACCCGT 474  
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
Db 475 CTAGCAGCTGATGTGGCAAGCTGGAGCTGAAGGGGAATTCAGAGGCTTTTGTGACTGC 534  
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
Db 535 CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCTGTACCAAGGCTTTTATGTGTCA 594  
QY 181 ValGlnGlylleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
Db 595 GTGAGGCGCAATATCATCTACCGTGTGCTTCTGCTATCTGATCTATGACACTGCAAGGGA 654  
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
Db 655 ATGCTCCGGATCCCAAGAAATCTACATCTTCATCAGCTGGATGATTGCACAGTCTGTC 714  
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
Db 715 ACTGCTGTGCTGCGCTAACTCTTATCTCTTTGACACCGTTCGCGGTGATGATGATG 774  
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
Db 775 CAGTCTGCAGCAGCAAGGAAGTATATCATGATATACAGGCAAGCTTGCCTGCGCGGAAG 834  
QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
Db 835 ATCGCTCGAGCAAGAGGAGGCAAGGCTTTTTCAGGGTGCATGTTCCAAACGTTCTCAGA 894  
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
Db 895 GGCATGGTGGTGGCTTTGCTTGTGATGATGAATCAAGAAAG 942

RESULT 13

US-10-403-571-153  
; Sequence 153, Application US/10403571  
; Publication No. US20040068763A1  
; GENERAL INFORMATION:  
; APPLICANT: HOPKINS, Nancy  
; APPLICANT: GOLLING, Gregory  
; APPLICANT: Amsterdam, Adam  
; APPLICANT: Sun, Zhaoxia  
; TITLE OF INVENTION: Developmental Mutations in Zebrafish  
; FILE REFERENCE: 01997/539002  
; CURRENT APPLICATION NUMBER: US/10/403,571  
; CURRENT FILING DATE: 2003-03-25



```
; PRIOR APPLICATION NUMBER: US 60/368,760
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-403-571-153

Alignment Scores:
Pred. No.: 6,79e-189 Length: 1243
Score: 1446.00 Matches: 274
Percent Similarity: 96.98% Conservative: 15
Best Local Similarity: 91.95% Mismatches: 3
Query Match: 93.71% Indels: 0
DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x US-10-403-571-153 (1-1243)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 45 ATGAGTGAGACCGCATCTCTTCCCAAGGACATCTTGGCCGCTGATTCGCCGCTGCC 104
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 105 ATCTCTAAACCGCGCTGGCCCATTTGAGAGAGTCAAACTGCTGCTTCAGGTGCAACAT 164
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 165 GCTAGCAACAGATACAGCAGATAGCAGTACAGGCGCATATGAGCTGCGTGGTGGT 224
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 225 ATCCCAAGGAGCGGGCTTCTGCTGTTCTGGAGAGAAACTTGGCCCAACGTCATCAGA 284
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 285 TACTTCCCAACAGCGCCCTCAACTTGTCTTCAAGGACAGTACAAAGAGGCTTCCCT 344
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 345 GATGTGTGGACAGCGCCACCTTTTGGAGGTACTTCGCTGTAACCTGGCTTCAGGT 404
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 405 GGTGTGCTGTGTCACATCCTCTGCTGTTGATCCCTTGACTTCGCAAGAACCCGT 464
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 465 CTGTGTCGCGAGTCGGAAGAGTCGACGAGAAAGAGAGTTCAGTGGCTGGGTAACTGC 524
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 525 TTGTAAGATCTCCAATCTGATGGCATCAAGGCTGTACCAAGGACTTCAACGTGCC 584
Qy 181 ValGlnGlyIleIleIleIleTyrAlaAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 585 GTGAGGGTATCATCATTTACAGAGCTGCCCTACTTCGGCATTTATGACACAGCAAGGGT 644
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 645 ATGTGCGCGATCCCAAGAACACCATATTTGTTGTGATGGATGATTTGCTCAGAGTGT 704
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 705 ACTGCTGTGTGCTCTTCTCTCTACCTACCTCTCGACACAGTGGCTCGTCTATGATGATG 764
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 765 CAGTCTGACGTAAGAGGCTGACATCATGTACAGTGGCACAATTAAGTCTCTCGAGGAG 824
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
; PRIOR APPLICATION NUMBER: US 60/368,760
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-403-571-153

Alignment Scores:
Pred. No.: 6,79e-189 Length: 1243
Score: 1446.00 Matches: 274
Percent Similarity: 96.98% Conservative: 15
Best Local Similarity: 91.95% Mismatches: 3
Query Match: 93.71% Indels: 0
DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x US-09-917-800A-1327 (1-1196)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 76 ATGGGGATCAGGCTTTCAGGCTTCTTAAGGACTTCTCGGAGGCTGCGATCGCCGCGCC 135
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 136 GTCCTCAAGACCGCGCTCGCCCGATCGAGAGGCTCAAACTGCTGCTGCTGAGGTCCAGCAT 195
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 196 GCCACCAACAGATCAGTGCAGAGAAACAGTACAAAGCATCATTTGTTGCTGCTGAGA 255
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
; PRIOR APPLICATION NUMBER: US 60/368,760
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 1243
; TYPE: DNA
; ORGANISM: Danio rerio
US-10-403-571-153

Alignment Scores:
Pred. No.: 6,97e-186 Length: 1196
Score: 1424.00 Matches: 267
Percent Similarity: 95.64% Conservative: 18
Best Local Similarity: 89.60% Mismatches: 13
Query Match: 92.29% Indels: 0
DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x US-09-917-800A-1327 (1-1196)
Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala 20
Db 76 ATGGGGATCAGGCTTTCAGGCTTCTTAAGGACTTCTCGGAGGCTGCGATCGCCGCGCC 135
Qy 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
Db 136 GTCCTCAAGACCGCGCTCGCCCGATCGAGAGGCTCAAACTGCTGCTGCTGAGGTCCAGCAT 195
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 196 GCCACCAACAGATCAGTGCAGAGAAACAGTACAAAGCATCATTTGTTGCTGCTGAGA 255
Qy 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
```



```
Db 256 ATCCCAAGGAGCAGGGCTTCTCTCCCTCTGGAGGGTAACCTGGCCAAAGTATCCGG 315
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 316 TACTTCCCACCACCAAGCTCTCAACTTCGCTTCAAGGACAAGTACAAGCAGATCTTCTG 375
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 376 GGAGGTGTGATCGTCGTCAAAGCAGTCTGGCGCTACTTCGCTGGTAACCTGGCTCTGGT 435
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 436 GGGGAGCTGGGGCTACCTCCCTCTGCTTCTGCTACCCCACTGGACTTTGCTAGACCCAGG 495
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGluPheArgGlyLeuGlyAspCys 160
Db 496 CTGGTGTGGCAGCTGGCGAAGGATCTTCCCAAGCGTGAGTTCAATGGGCTGGGTCAGCTGT 555
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 556 CTCACCAAGATCTTCAAGCTGATCGCTGAGGCTGAAGGCTCTTACCAGGTTTCAGTGTCTCT 615
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 616 GTCCAGGGCATCATCATCTACAGAGCTGCTACTTCGGAGTCTATGACACTGCCAAGGGG 675
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 676 ATGCTGCCAGACCCCAAGATGTGCACATTAATGTGAGCTGATGATTCACCAAGTGTG 735
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 736 ACAGCCGTGGGGGCTGGTGCTCTCATTTTGACACTGTCCTCGTGTAGATGATGATG 795
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 796 CAGTCTGGCCGAAGAGGGCTGATATATGATATACACGGGACAGTGTGACTGCTGGAGGA 855
Qy 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyValAlaTrpSerAsnValLeuArg 280
Db 856 ATTCGAAGATGAGAGCGCAAGCTTCTCAAGGTGCTTGTGCCAAGCTACTGAGA 915
Qy 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValle 298
Db 916 GCATGGGGGGTCTTTGTATTGTATTGTATGATGATGATGATGATGATGATGATG 969
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## RESULT 15

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US-10-198-846-13437
; Sequence 13437, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13437
; LENGTH: 1711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 2, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405,
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; LOCATION: 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415,
; LOCATION: 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425,
; LOCATION: 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444,
; LOCATION: 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13437
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## Alignment Scores:

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Pred. No.: 1,43e-183 Length: 1711
Score: 1409.00 Matches: 263
Percent Similarity: 94.63% Conservative: 19
Best Local Similarity: 88.26% Mismatches: 16
Query Match: 91.32% Indels: 0
DB: 15 Gaps: 0
```

US-09-811-094-33 (1-298) x US-10-198-846-13437 (1-1711)

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Qy 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaA 20
Db 167 ATGGGTGATCACCGCTTGGAGCTTCTTAAAGGATCTTCGGCCGGGGCGCTCGCGTGC 226
Qy 21 IleSerLysThrAlaValAlaAlaProIleGluArgValLysLeuLeuGlnHis 40
Db 227 GTCTCCAAGACCGGGTGGCCCCCATCGAGAGGGTCAAACTGCTGCTGCAGGTCCAGCAT 286
Qy 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 287 GCCAGCAACAGATCATGCTGAGAGGAGTACAAAGGGATCATATTGATTGTGTGTGAGA 346
Qy 61 IleProLysGlnGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
Db 347 ATCCCTAAGAGCAGGGCTTCTCTCTCTGAGGGGTAACTGCGCCACGATGATCCGT 406
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 407 TACTTCCCCACCAAGCTCTCAACTTCGCCCTTCAAGGACAAGTACAAAGCAGCTCTCTTA 466
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 467 GGGGGTGTGATCGGATACAGAGTCTGCGCTACTTTGCTGTTAACTTGGGCTCGGT 526
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 527 GGGGCCGCTGGGGCCACTCCCTTTGCTTTGCTTCTACCGCTGACCTTGTAGACACAG 586
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 587 TTGGCTGCTGATGTGGCAAGGGCGCGCCCGCCAGCGTGAGTTCATGCTTGGGCGACTGT 646
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
Db 647 ATCATCAAGATCTTCAAGTCTGATGGCTGAGGGGGGCTCTACCGAGGTTCACAGTCTCT 706
Qy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
Db 707 GTCCAGGCATCATATTATATAGAGCTGCTACTTCCGAGTCTATGATATCTGCAAGGGG 766
Qy 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
Db 767 ATGCTGCTGACCCCAAGAACGTCACATTTTGTGAGCTGGATGATTTGCCAGAGGTG 826
Qy 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
Db 827 ACGGCAGTCCAGGGCTGGTGTCTTACCCCTTTTGACACTGTTCTGCTGATGATGATG 886
Qy 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
Db 887 CAGTCCGGCCGAAGGGCGCATATTATGTATACCGGGGACAGTTGACTGCTGGAGGAAG 946
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QY      261  IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValIleuArg 280
Db      947  ATTGCAAAAGACGAAGGAGCCAGGCCCTTCTTCAAGGTGGCTGGTCCAAATGTCGTGAGA 1006

QY      281  GlyMetGlyGlyAlaPheValIleuValLeuTyrAspGluLeuLysLysValIle 298
Db      1007  GGCATGGCGGTGCTTTTGTATTGGTGTGTATGATGATGATCAAAAAAATATGTC 1060
```

Search completed: August 17, 2004, 21:40:56  
Job time : 543 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 17, 2004, 17:56:49 ; Search time 2930 Seconds  
(without alignments)  
3037.177 Million cell updates/sec

Title: US-09-811-094-33  
Perfect score: 1543  
Sequence: 1 MTEQAISPAKDFLAGGIAAA.....LRMGAGFVLVLYDELKKVI 298

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q/cgn2.1/USPTO spool/US09811094/runat 10082004.105413.12472/app\_query.fasta.1.455  
-DB=EST -OPMT=fastop -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR SCORE=act -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pcr -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09811094 @CNC\_1\_3437 @runat 10082004.105413.12472 -NCPU=6 -ICPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estro.\*  
8: em\_hic.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hic.\*  
12: gb\_est3.\*  
13: gb\_est4.\*  
14: gb\_est5.\*  
15: em\_estfun.\*  
16: em\_estom.\*  
17: em\_gss\_hum.\*  
18: em\_gss\_inv.\*  
19: em\_gss\_pln.\*  
20: em\_gss\_vrt.\*  
21: em\_gss\_fun.\*  
22: em\_gss\_mam.\*  
23: em\_gss\_mus.\*  
24: em\_gss\_pro.\*  
25: em\_gss\_rod.\*  
26: em\_gss\_pbg.\*  
27: em\_gss\_vrl.\*  
28: gb\_gssi.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1543	100.0	1355	11	BC013256	BC013256 Homo sapi
2	1543	100.0	1355	11	BC035469	BC035469 Homo sapi
3	1474	95.5	1201	13	EX419742	EX419742 BX419742
4	1463	94.8	1201	13	EX353661	EX353661 BX353661
5	1458	94.5	1201	9	AL545701	AL545701 AL545701
6	1454.5	94.3	1201	9	AL534908	AL534908 AL534908
7	1452.5	94.1	1071	12	BM554606	BM554606 AGENCOURT
8	1451	94.0	949	13	BQ932832	BQ932832 AGENCOURT
9	1451	94.0	1218	14	CF110898	CF110898 Shultzomi
10	1449	93.9	1201	9	AL540267	AL540267 AL540267
11	1445	93.6	1237	11	AK012951	AK012951 Mus muscu
12	1445	93.6	1237	11	AK088730	AK088730 Mus muscu
13	1445	93.6	1239	11	AK003467	AK003467 Mus muscu
14	1440	93.3	1015	13	BX360934	BX360934 BX360934
15	1438	93.2	1064	14	CK024940	CK024940 AGENCOURT
16	1436	93.1	1185	9	AL515693	AL515693 AL515693
17	1435	93.0	1130	14	CF660610	CF660610 CCLX07a30
18	1434	92.9	1201	13	BX424943	BX424943 BX424943
19	1432	92.8	1145	14	CK025379	CK025379 AGENCOURT
20	1432	92.8	1201	13	BX395578	BX395578 BX395578
21	1431	92.7	1045	13	BX420955	BX420955 BX420955
22	1428	92.5	1160	14	CK025422	CK025422 AGENCOURT
23	1426	92.4	1171	14	CF111068	CF111068 Shultzomi
24	1421	92.1	911	13	EX708727	EX708727 BX708727
25	1418	91.9	1201	9	AL557414	AL557414 AL557414
26	1418	91.9	1201	13	BX462646	BX462646 BX462646
27	1417	91.8	1106	14	CK025329	CK025329 AGENCOURT
28	1416	91.8	1201	9	AL539376	AL539376 AL539376
29	1414	91.6	1295	11	AK078077	AK078077 Mus muscu
30	1410	91.4	959	13	BX705948	BX705948 BX705948
31	1410	91.4	1006	13	EX704347	EX704347 BX704347
32	1405	91.1	1014	13	BX375536	BX375536 BX375536
33	1404	91.0	937	13	BX706933	BX706933 BX706933
34	1404	91.0	1090	13	BX457520	BX457520 BX457520
35	1400	90.7	931	13	BQ933670	BQ933670 AGENCOURT
36	1400	90.7	1201	9	AL514420	AL514420 AL514420
37	1398	90.6	1119	13	BUS15488	BUS15488 AGENCOURT
38	1396	90.5	1209	14	CD496256	CD496256 CDA21-C08
39	1394	90.3	956	13	EX703901	EX703901 BX703901
40	1393	90.3	1201	13	BX464683	BX464683 BX464683
41	1392	90.2	1236	11	AK002283	AK002283 Mus muscu
42	1390	90.1	921	13	BX708871	BX708871 BX708871
43	1390	90.1	999	13	EX411074	EX411074 BX411074
44	1389	90.0	1146	14	CD509246	CD509246 CDA95-C07
45	1388	90.0	931	13	BX728888	BX728888 BX728888

# ALIGNMENTS

RESULT 1  
BC013256

LOCUS

DEFINITION

BC013256 1355 bp mRNA linear HTC 17-DEC-2003  
Homo sapiens solute carrier family 25 (mitochondrial carrier;  
adenine nucleotide translocator), member 6, mRNA (cDNA clone  
IMAGE:3865895).

ACCESSION

BC013256

VERSION

BC013256.1

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE  
AUTHORS

1 (bases 1 to 1355)  
 Strausberg R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
 Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
 Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,  
 Scheetz, J.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,  
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
 Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,  
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Rulyk, S.W.,  
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
 Fahy, J., Hellon, E., Kettman, M., Madan, A., Rodrigues, S.,  
 Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E.,  
 Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 12477932

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

2 (bases 1 to 1355)  
 Strausberg, R.  
 Direct Submission  
 Submitted (27-AUG-2001) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 13 Row: e Column: 10  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 4507746  
 This clone has the following problem: no 5' EST match.

## FEATURES

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 /clone="IMAGE:3865895"  
 /tissue\_type="Eye, retinoblastoma"  
 /clone\_lib="NIH MGC\_67"  
 /lab\_host="DH10B"  
 /note="vector: pCMV-SPORT6"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1.43e-179 Length: 1355  
 Score: 1543.00 Matches: 298  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 11 Gaps: 0

US-09-811-094-33 (1-298) x BC013256 (1-1355)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyLeuAlaAa 20  
 Db 92 ATGACGGAACAGGCCATCTCTTCGCAAGACTTCTTGGCGGAGGCATCGCGCGCC 151  
 QY 21 ILeSerIysThrAlaValAlaProIleGluArgValLysLeuLeuGlnHis 40  
 Db 152 ATCTCAAGACGCGCGTGGTCCGATCGAGCGGGTCAAGCTGCTGAGGTCCAGCAC 211  
 QY 41 AlaserLysGlnIleAlaAlaLysGlnIleLysGlyValValAspCysIleValArg 60  
 Db 212 GCCAGCAAGCAGATCGCCGCCAGCAGTAGTCAAGGGCATCGTGACTGCATTCGCG 271  
 QY 61 ILeProIysGluGlnIleValLeuSerPheThrArgGlyAsnLeuAlaValIleArg 80  
 Db 272 ATCCCCAAGAGCAGGGCGTGTCTCTTCGAGGGGCAACCTTGCACACGTCATTCGC 331  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
 Db 332 TACTTCCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAGTACAGCAGATCTTCCTG 391  
 QY 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
 Db 392 GGGGGCGTGGACAAAGCACACGCGAGTTCTGGAGGTACTTTGCGGGCAACCTGGCCCTCGCGC 451  
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaThrArg 140  
 Db 452 GTGTGGCGCGCGCGACCTCTCTGCTTGTGTACCCCTCGATTTGCCCAACACCGCG 511  
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
 Db 512 CTGGCAGCGGACGTTGGGAAAGTCAGGCACAGACGCGAGTTCGAGGCGCTGGAGACTGC 571  
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
 Db 572 CTGGTGAAGATCACCAGTCCCGACCGCATCCGGCGCTGTACCGGGGTTTGTAGTCTCC 631  
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200  
 Db 632 GTGAGGGCATCATCATCTACCGGGCGCTACTTTCGGCGTGTACGATACGGCCAGGGC 691  
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220  
 Db 692 ATGCTCCCGACGCCCAAGAACACGACATCGTGTGAGCTGAGCTGATCGCGCAGACCGTG 751  
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 Db 752 AGCGCGTGGCGCGGTGGTGTCTTACCCCTTCGACAGCGTGGCGCGGCGATGATGATG 811  
 QY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260  
 Db 812 CAGTCCGGCGCGCAAGAGAGTGCATCATGTACACGGGCACCGTGCAGTGTGGAGGAAG 871  
 QY 261 ILePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280  
 Db 872 ATCTTCAGATGAGGGGGGCAAGCCCTTTCAGAGGTGGTGTGTCACAGCTCTCGCGG 931  
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle 298  
 Db 932 GGCATGGGGGGCGCTTCGTGCTGCTCTGTACGACGAGCTCAAGAGAGTGTATC 985

## RESULT 2

BC035469  
 LOCUS  
 DEFINITION  
 Homo sapiens solute carrier family 25 (mitochondrial carrier;  
 adenine nucleotide translocator), member 6, mRNA (cDNA clone  
 IMAGE:3867130).  
 ACCESSION  
 BC035469  
 VERSION  
 BC035469.1 GI:22028373  
 KEYWORDS  
 HTC.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE	1 (bases 1 to 1355)	QY	1	MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAala	20
AUTHORS	Klausner,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Schenker,C.M., Schuler,G.D., Altshul,S.F., Zeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diachenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stalteron,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahy,J., Helton,E., Kertanen,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickinson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smallus,D.E., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.	Db	92	ATGACGGAAAGGCGCATCTCTTCGCCAAAGACTTCTTGGCCGGAGGACATCGCGCGCC	151
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	QY	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 15899-15903 (2002)	Db	152	ATCTCCAAGACGGCGGTGGCTCCGATCGAGCGGTCAAGCTGCTGCTGAGGTCCAGCAC	211
PUBLISHED	12477932	QY	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrlsGlyIleValAspCysIleValArg	60
AUTHORS	Strausberg,R.	Db	212	GCCAGCAGCAGATCGCGCGGCAACAGCAGTACAAAGGGCATCGTGGACTCATTTGTCGC	271
TITLE	Direct Submission	QY	61	IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
JOURNAL	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 1A03, Bethesda, MD 20892-2590, USA	Db	272	ATCCCCAAGGAGCGGCGGTGCTGCTCTTGGAGGGGCAACCTTGCACAGTCATTCGC	331
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrlsGlnIlePheLeu	100
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a> Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LINL) Sequencing Center Center code: BCM-HGSC Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a> Contact: <a href="mailto:ang@bcm.tmc.edu">ang@bcm.tmc.edu</a> Gunsaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Lousseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	Db	332	TACTTCCCACTCAAGCCCTCACTTCGCCCTCAAGGATAAGTACAGAGAGATCTTCCTG	391
		QY	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrlsGlyAsnLeuAlaSerGly	120
		Db	392	GGGGCGGTGGACAAGCAGCAGCTTCTGGAGGTACTTTGGGGCAACCTTGGCTCGGC	451
		QY	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrlsPheLeuAspPheAlaArgThrArg	140
		Db	452	GGTGGCGCGCGGCGACCTCCCTCTGCTTGTGTACCCGCTGGATTTTCGACAGACCCGC	511
		QY	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
		Db	512	CTGCGACGGACGTGGGAAAGTACAGGCAGAGCGCGAGTTCGAGGCTTGGAGACTGC	571
		QY	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrlsGlnGlyPheSerValSer	180
		Db	572	CTGTGAAGATCAACCAAGTCGACGGCATCCGGGGCTGTACACAGGCTTCAGTGTCTCC	631
		QY	181	ValGlnGlyIleIleIleTyrlsArgAlaAlaTyrlsPheGlyValTyrlsAspThrAlaLysGly	200
		Db	632	GTGCAGGGCATCATCATCTACCGGCGGCTTCTCGCGGTGTACGATACGCGCAAGGCG	691
		QY	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
		Db	692	ATGCTCCCGACCCCAAGAACACGACATCGTGTGTGAGCTGGATGATCGGCACACCGTG	751
		QY	221	ThrAlaValAlaGlyValValSerTyrlsPheAspThrValArgArgMetMetMet	240
		Db	752	ACGGCGGTGGCGCGGTGTCTTACCCCTTCACACCGGTGCGCGCGCATCATGATG	811
		QY	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrlsThrGlyThrValAspCysTrpArgLys	260
		Db	812	CAGTCCGGCGCAAGGAGCTGACATCATGTACACGGGACCGCTCGACTGTTGGAGGAG	871
		QY	261	IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg	280
		Db	872	ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGTTGCTGCTCAACGCTCTCGCG	931
		QY	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrlsAspGluLeuLysLysValIle	298
		Db	932	GGCATGGGGCGCGCTTCTGCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	985
FEATURES	source	RESULT 3			
		LOCUS	BX419742	1201 bp	mRNA linear EST 13-MAY-2003
ORIGIN		DEFINITION	BX419742 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone		
		ACCESSION	CS0DF020YC16 5-PRIME, mRNA sequence.		
		VERSION	BX419742		
		KEYWORDS	EST.		
		SOURCE	EST.		
		ORGANISM	Homo sapiens (human)		
			Homo sapiens		
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
		REFERENCE	1 (bases 1 to 1201)		

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.lnl.gov>  
Series: IRAX Plate: 13 Row: f Column: 9  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4503556  
This clone has the following problem: no 5' EST match.

Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGES:3867130"  
/tissue types="Eye, retinoblastoma"  
/clone lib="NIH MGC 67"  
/lab host="DH10B"  
/note="Vector: pCMV-SPORTs"

## ORIGIN

## Alignment Scores:

Pred. No.: 1,43e-179 Length: 1355  
Score: 1543.00 Matches: 298  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 11 Gaps: 0

US-09-811-094-33 (1-298) x BC035469 (1-1355)

QY	161	LeuValIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 18
Db	632	CTGCTGAAGATCACCAAGTCCGACGCATCCGGGCGTGTACAGGGGTTCACTGCTCTCC 691
QY	181	ValGlnGlyIleIle-IleTyrArgAlaIleTyrPheGlyValTyrAspThrAlaLysG 20
Db	692	GTGACGGGATCATCATCTACCGGCGCCCTACCTTCGGCGGTGTACGATACGCCCAAGG 751
QY	200	yMetLeuProAspProLysAsnThrHisIleValValSerTTPMetIleAlaGlnThrVa 220
Db	752	CATGCTCCCGACCCCAAGAACACGCACATCGTGGTGTAGCTGATGATCGCGACACGCT 811
QY	220	lThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMe 240
Db	812	GACGGCGGTGGCGGCGTGTGCTTACCCCTTCGACACGGTGGCGGCGCGCATGATGAT 871
QY	240	tGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTTPArgLy 260
Db	872	GCACTCGGGCGCAAGAGAGCTGACATCATGTACAGGGCAGCTGGACTGTTGGAGGNA 931
QY	260	sllePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTTPSerAsnValLeuAr 280
Db	932	GATCTTTACAGATGAGGGGCAAGCCCTTCTTAAGGGTGGTGGTCCCAAGCTCCTCGC 991
QY	280	SGlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlyLeuLysLysValIle 298
Db	992	GGCATGGGGGGGGCTTCTGCTGCTGTGTACACGAGCTCAARAAGGTGATC 1046
RESULT 4		
QY	BX353661	1201 bp mRNA linear EST 05-MAY-2003
Db	BX353661	Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
QY	DEFINITION	CDNA clone CS0DC010YK03 5-PRIME, mRNA sequence.
Db	ACCESSION	BX353661
QY	VERSION	BX353661.1 GI:30375795
Db	KEYWORDS	EST.
QY	SOURCE	Homo sapiens (human)
Db	ORGANISM	Homo sapiens
QY	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Db	AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
QY	TITLE	Full-length cDNA libraries and normalization
Db	JOURNAL	Unpublished (2001)
QY	COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DF020B08QPl&cluster=10389.r. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DF020B08QPl. Location/Qualifiers 1. .1201 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DF020YCl6" /tissue_type="FETAL BRAIN" /dev_stage="fetal" /clone_lib="Homo sapiens FETAL BRAIN" /note="Organ: Brain; Vector: pCMVSPORT_6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
ORIGIN		
QY	Alignment Scores:	
Db	Pred. No.:	4,11e-171 Length: 1201
QY	Score:	1474.00 Matches: 292
Db	Percent Similarity:	97.66% Conservative: 0
QY	Best Local Similarity:	97.66% Mismatches: 6
Db	Query Match:	95.53% Indels: 2
QY	DB:	Gaps: 0
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Db	153 ATGACGGACAGCCATCTCTTCCCAAAATTTCTTGGCGGAGS-ATCGMGCCGCM 211	
QY	21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40	
Db	212 ATCTCCAAGACGGCGTGGCTCCGATCGAGCGGGTCAAGCTGCTGTCAGGTCCAGCAC 271	
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Db	272 GCACAGACAGATCGCCGCCAAGACAGTACAGGACATCTGGATGCTATGTCGCG 331	
QY	61 IleProLysGluGlnGlyValLeuSerPheThrArgGlyAsnLeuAlaAsnValIleArg 80	
Db	332 ATCCCAAGGACAGGGCGTGTCTCTTCTGGAGGGCAACCTTGCMAAGTCAATTCGC 391	
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QY	121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140	
Db	512 GGTGCGGCGCGCGAMCTCCCTCTGCTGTGTACCGCTGGATTTGCCAGAACCCGC 571	
QY	141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160	
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Alignment Scores: Pred. No.: 9,46e-170 Length: 1201 Matches: 1463.00 Score: 275		

Alignment Scores:  
Pred. No.: 9,46e-170 Length: 1201  
Score: 1463.00 Matches: 275

Percent Similarity: 97.30%		Conservative: 13	
Best Local Similarity: 92.91%		Mismatches: 8	
Query Match: 94.82%		Indels: 0	
DB: 13		Gaps: 0	
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DB	128	ATGACAGATGCCGTGTGCTTCCGCAAGGACTTCTGCGAGGTGGAGTGGCCGACGCC	187
QY	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
DB	188	ATCTCCAAAGCCGGGTAGCGCCATCGAGCGGGTCAAGCTCTCTGCGAGTGCAGCAT	247
QY	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
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QY	61	IleProLysGluGlnGlyValLeuSerPheTyrArgLysAsnLeuAlaAsnValIleArg	80
DB	308	ATTCCCAAGAGCAGGAGGTCTGTCTCTGCGCGGTAACTGGCCAAATGTCATCAGA	367
QY	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
DB	368	TACTTCCCAACCCAGGCTTTAACTTCGCTTCAAGATAAATACAGCAGATCTTCCTG	427
QY	101	GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly	120
DB	428	GGTGGTGTGGACAAAGAACCCAGTTTGGCGCTACTTTGCAGGGAATCTGGCATCGGT	487
QY	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg	140
DB	488	GGTGGCGGAGGGGCCACATCCCTGTGTTTGTGTACCCCTCTGTATTTGCCGTACCCGT	547
QY	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
DB	548	CTAGCAGCTGATGTGGTAAACTGGAGCTGAAGGGAAATTCGAGGCCCTCGTCACTGC	607
QY	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer	180
DB	608	CTGGTTAAGATCTACAAATCTGATGGGATTAAGGGCTGTACCAAGGCTTTAAGTGTCT	667
QY	181	ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly	200
DB	668	GTGCAGGTAATATCATCTACCGAGCGGCTACTTCGGTATCTATGACACTGCAAGGA	727
QY	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
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QY	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet	240
DB	788	ACTGCTGTGCGGGTGTGACTTCCTATCCATTTGACACCGTTCGCGCGCATGATGATG	847
QY	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
DB	848	CAGTCAGGCGCAAGGAAGTACATCATGTACACAGGCACCGTTGACTGCTGGCGGAAG	907
QY	261	IlePheArgAspGlnGlyLysAlaPhePheLysGlyAlaTrpSerAsnValIleArg	280
DB	908	ATTGCTCGTATGAAGAGGCAAGCTTTTTCATAGGCGTGCATGTGTCCTCAATGTC	967
QY	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys	296
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RESULT 5			
AL545701			
LOCUS			
DEFINITION			
AL545701 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA			
clone CSODI009H03 5-PRIME, mRNA sequence.			
ACCESSION			
AL545701			

AL545701.2 GI:31267536	
EST.	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
1 (bases 1 to 1201)	
Li.W.B., Gruber,C., Jesse,J. and Polayes,D.	
Full-length cDNA libraries and normalization	
Unpublished (2001)	
On Feb 15, 2001 this sequence version replaced gi:12878183.	
Contact: Genoscope	
Genoscope - Centre National de Sequencage	
BP 191 91006 EVRY cedex - France	
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr	
Library was constructed by Life Technologies, a division of	
Invitrogen. This sequence belongs to sequence cluster 10389.r For	
more information about this cluster, see	
http://www.genoscope.cns.fr/	
cgi-bin/cluster.cgi?seq=CSODI009CD02QP1&cluster=10389.r. Contact :	
Feng Liang Email : fliang@lifetech.com URL :	
http://fulllength.invitrogen.com/Invitrogen Corporation 1600	
Faraday Avenue Genoscope sequence ID : CSODI009CD02QP1.	
Location/Qualifiers	
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/organism="Homo sapiens"	
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/note="First strand cDNA was primed with a NotI-oligo(dT)	
primer. Five prime end enriched, double-strand cDNA was	
digested with Not I and cloned into the Not I and EcoR V	
sites of the pCMVSPORT 6 vector. Library was normalized."	

ALIGNMENT SCORES:			
Pred. No.:	3,93e-169	Length:	1201
Score:	1458.00	Matches:	290
Percent Similarity:	97.32%	Conservative:	1
Best Local Similarity:	96.99%	Mismatches:	5
Query Match:	94.49%	Indels:	3
DB:	9	Gaps:	0
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QY	22	SerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAla	41
DB	111	TCCAAGCGCGGTGGCTCCGATCGAGCGGTCAAGCTGCTGCTCAGGTCACACGCC	170
QY	42	SerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArgIle	61
DB	171	AGCAAGCAGATCGCGCGCACAGCAGTACAAAGGCATCTGTTGACTCATTTGCCGATC	230
QY	62	ProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArgTyr	81
DB	231	CCCAAGAGCAGCGCGCTGCTCTCTTGGAGGGGCAACCTTGGCAACGTCATTCGTAC	290
QY	82	PheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeuGly	101
DB	291	TTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAAGCAGATCTTCCTGGG	350
QY	102	GlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGlyGly	121
DB	351	GGCGTGGACCAAGCACCGCAGTCTCTGGAGGTACTTTTGGGCAACCTTGGCTCCGGCGGT	410
QY	122	AlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArgLeu	141

VERSION		AL545701.2		GI:31267536	
KEYWORDS		EST.			
SOURCE		Homo sapiens (human)			
ORGANISM		Homo sapiens			
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
TITLE		Li, W.B., Gruber, C., Jessee, J. and Polayes, D.			
JOURNAL		Full-length cDNA libraries and normalization			
COMMENT		Unpublished (2001)			
		On Feb 15, 2001 this sequence version replaced gi:12878183.			
		Contact: Genoscope			
		Genoscope - Centre National de Sequencage			
		BP 191 91006 EVRY cedex - France			
		Email: seqraf@genoscope.cns.fr, Web : www.genoscope.cns.fr			
		Library was constructed by Life Technologies, a division of			
		Invitrogen. This sequence belongs to sequence cluster 10389.r for			
		more information about this cluster, see			
		http://www.genoscope.cns.fr/			
		cgi-bin/cluster.cgi?seq=CSODI009CD02QP1&cluster=10389.r. Contact :			
		Feng Liang Email : fliang@lifetech.com URL :			
		http://fulllength.invitrogen.com/ Invitrogen Corporation 1600			
		Paraday Avenue Genoscope sequence ID : CSODI009CD02QP1.			
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		/note="1st strand cDNA was primed with a NotI-oligo (GT			
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		sites of the pCMVSPORT 6 vector. Library was normalized."			
ORIGIN					
Alignment Scores:					
Pred. No.:		3,93e-169		Length:	
Score:		1458.00		Matches:	
Percent Similarity:		97.32%		Conservative:	
Best Local Similarity:		96.99%		Mismatches:	
Query Match:		94.49%		Indels:	
DB:		9		Gaps:	
US-09-811-094-33 (1-298) x AL545701 (1-1201)					
QY	2	ThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaIle	21		
DB	51	TCCCGGGATGCCATCTCTTCCGCAAGACTTCTTGGCGGACGCTNCGCGCGCCATC	110		
QY	22	SerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAla	41		
DB	111	TCCAAGACGGCGGTGCTCGATCGAGCGGTCAAGCTGTCTGTCAGGTCCAGCAGCC	170		
QY	42	SerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArgIle	61		
DB	171	AGCAAGCAGATCGCGCGCCACAGCAGTACAAAGGCACTCGTGGACTCAITTCGCA	230		
QY	62	ProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArgTyr	81		
DB	231	CCCAGGAGCAGCGGTGCTCTCTTGGAGGGGCAACCTTGGCAACGCTTCITTCGCTAC	290		
QY	82	PheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeuGly	101		
DB	291	TTCCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAAGCAGATCTTCTGGG	350		
QY	102	GlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGlyGly	121		
DB	351	GGCTGGCAACAGCACGCGAGTTCCTGGAGGTACTTTTGGGGCAACCTGGCGCGGT	410		
QY	122	AlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArgLeu	141		

Db 411 GCGGCGGCGGACCTCTCTGCTTGTGTACCGCTGGATTTCCGCAAGAACCCGCTG 470

QY 142 AlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCysLeu 161

Db 471 GCAGCGAGCTGGAAAGTCAGGCACAGAGCGGAGTTCGAGAGCTGGAGACTGCTG 530

QY 162 ValValIleThrLysSerAspGlyLeuArgGlyLeuThrGlnGlyPheSerValSerVal 181

Db 531 GTGAAGATCACCAAGTCCGACGACATCGTGGTGTGTACCAAGGCTTCAGTGTCTCCGTG 590

QY 182 GlnGlyIleIleLeuArgAlaAlaValPheGlyValThrAspThrAlaLysGlyMet 201

Db 591 CAGGGCATCATCTACCGGCGGCTACTTCGGCGGTGTACATACGCGCAGGCGCATG 650

QY 202 LeuProAspProLysAsnThrHisLeuValSerTrpMetIleAlaGlnThrValThr 221

Db 651 CTCGCCGACCCCAAGAACACGACATCGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGT 710

QY 222 AlaValAlaGlyValValSerTrpPheAspThrValArgArgMetMetMetGln 241

Db 711 GCGGTGGCGGCGGTGTGTCTACCCCTTCGACAGGTGGCGCGCGCATGTATGTCAG 770

QY 242 SerGlyArgGlyGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgLysIle 261

Db 771 TCCGGCGGCAAGAGAGCTGACATCATGTATACCGGCGCAGTTC - GACTGTTGGAGGAGATC 829

QY 262 PheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArgGly 281

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Db 890 CATGGCGGCGGCGCTCTGT 942

RESULT 6

AL534908 1201 bp mRNA linear EST 12-MAY-2003

LOCUS AL534908 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone

DEFINITION CS0DF007Y120 5-PRIME, mRNA sequence.

ACCESSION AL534908

VERSION AL534908.2 GI:30541165

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 13, 2001 this sequence version replaced gi:12798401.

Contact: Genoscope

Genoscope - Centre National de Sequencage

Bp 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 10389.r For more information about this cluster, see

http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DF007BE10P1&cluster=10389.r. Contact:

Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID: CS0DF007BE10Q1.

Location/Qualifiers

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/note="Organ: brain; Vector: pCMVSPORT\_6; 1st strand cDNA"

FEATURES

source

was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

## ORIGIN

Alignment Scores: Length: 1201

Pred. No.: 1,07e-168 Matches: 293

Score: 1454.50 Conservative: 0

Percent Similarity: 97.99% Mismatches: 5

Best Local Similarity: 97.99% Indels: 3

Query Match: 94.26% Gaps: 0

DB: 9

US-09-811-094-33 (1-298) x AL534908 (1-1201)

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Db 161 ATGACGGAACAGGCGCATCTCTTCGCAAGACTTCTTGGCGGAS--ATCGCGCGCGCC 218

QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnHis 40

Db 219 ATCTCCAAGACGCGCGTGTCTCCGATCGASCAGGTCAAGCTGTCTGTGAGGTCCAGCAC 278

QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60

Db 279 GCCAGCAGCAGATCCCGCCGACAGCAGTACAGGGCATCTGTGAGCTGCATTGTCCGC 338

QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80

Db 339 ATCCCAAGAGCAGCGCGTGTCTCTTCGAGGGGCAACCTTGGCGGCAACCTGGCCCTCCGCG 398

QY 81 TrpPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100

Db 399 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAGCAGATCTTCTCTG 458

QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTrpPheAlaGlyAsnLeuAlaSerGly 120

Db 459 GGGGGCGGTGGACAAAGCACACGACAGTTCGAGGTACTTTCGGGGCAACCTGGCCCTCCGCG 518

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QY 181 ValGlnGlyIleIleLeuTrpArgAlaAlaTrpPheGlyValTrpAspThrAlaLysGly 200

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QY 201 MetLeuProAspProLysAsnThrHisLeuValSerTrpMetIleAlaGlnThrVal 220

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QY 221 ThrAlaValAlaGlyValValSerTrpPheAspThrValArgArgMetMetMet 240

Db 819 ACGGCGGTGGCGGCTGGGTGTCTTATCTCTTCGACAGCGTTCGGCGCGCATGTATGATG 878

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Db 879 CAGTCCGCGCGCAAGAGGAGCTGACATCATGTATACCGCGCACGTC - GACTGTTGGAGGAAG 937

QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280

Db 938 ATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGTGTGTGTGTGTGTGTGTGTGTGT 997

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## ORIGIN

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Score: 1451.00 Matches: 285
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Best Local Similarity: 95.64% Mismatches: 7
Query Match: 94.04% Indels: 2
DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BQ932832 (1-949)

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DB 53 ATGACGGAGACGACATCTCTCCCAAGACTTCTTGGCGGAGGATCGCGCGGCC 112
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DB 113 ATCTCCAGACGGCGTGGCTCCGATCGCGGGTCAGCTGCTGCTGCAGTCCAGCAC 172
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValarg 60
DB 173 GCCAGCAAGCAGATCGCGCGGACAGCAGTACAGGCGCATCGTGGACTGCTGCCGC 232
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DB 233 ATCCCAAGGACGAGGGGTGCTCTCTCTTGGAGGGCACTTGGCAAGTCAATTCGC 292
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 293 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGGATAAGTACAAGCAGATCTTCTG 352
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DB 413 GGTGGCGCGCGGACCTCCCTCTGCTTCTGTATACCGCTGGATTCGCCAGAACCGCG 472
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 473 CTGGCAGCGGACGTGGGAACTCAGGCACAGAGCGCGAGTTCGAGGCTGGGAGATGC 532
QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValser 180
DB 533 CTGGTGAGATCACCAGTCCGAGCGGATCCGGGCGCTGTACCAAGGCTTCAGTGTCTCC 592
QY 191 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 593 GTGCAGGGCATCATCATACCGCGCGGCTTCTTCCGCGGTGTACGATACGGCCAGGGC 652
QY 201 MetLeuProAspProLysAsnThrHisTyrValValSerTrpMetIleAlaGlnThrVal 220
DB 653 ATGCTCCCGACCCCAAGACAGCAGCATCTGTGTAGCTGGATGATCGCGCAGACCGTG 712
QY 221 ThrAlaValAlaGlyValValserTyrProPheAspThrValArgArgMetMetMet 240
DB 713 ACGGCGGTGGCGCGGTGTCTTACCTTCCACCGGTGGCGCGCGCGCATGATGATG 772

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QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCys-TrpArgLys 260
DB 773 CAGTCCCGGCGCAAGAGAGTGCATCATGTATACAGGGCACCGTGCAGCTGTGGAGGAA 832
QY 260 sIlePheArgAspGlyGlyGlyAlaPhePheLysGlyAlaTrpSerAsnValLeuAr 280
DB 833 GATCTTCANAGATGAGGGGGGAGGGCCCTCTTCAAGGTGGTGGTCCACCTCTCGNG 892
QY 280 GGLMetGlyGlyAla-PheValLeuValLeuTyrAspGluLeuLysLys 296
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## RESULT 9

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CF110898 1218 bp mRNA linear EST 23-JUL-2003
LOCUS Shultzomica04149 Rat lung airway and parenchyma cDNA libraries
DEFINITION Rattus norvegicus cDNA clone Contig3683 5', mRNA sequence.
ACCESSION CF110898
VERSION CF110898.1 GI:33167221
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

```

## REFERENCE

```

1. (bases 1 to 1218)
Shultz,M.A., Zhang,L., Gu,Y.-Z., Baker,G.L., Fannuchi,M.V.,
Padua,A.M., Gurske,W.A., Morin,D., Penn,S.G., Jovanovich,S.B.,
Plopper,C.G. and Buckpitt,A.R.
Gene Expression Analysis in Response to Lung Toxicants: I.
Sequencing and Microarray Development
Unpublished (2003)
Contact: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA
Tel: 530 752 0793
Fax: 530 752 4698
Email: mshultz@ucdavis.edu

```

## AUTHORS

```

Average Phred score is 20 or better. All poor quality data (Phred <
20) and vector/linker sequence has been removed.
High quality sequence stop: 1218.
Location/Qualifiers
1. 1218
/organism="Rattus norvegicus"
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/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/notes="Organ: lung; Vector: pGEM-lizf(-); Site 1: Eco RI;
Site 2: Not I; mRNA was isolated from microdissected rat
lung airways and parenchyma tissues."

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## JOURNAL

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COMMENT

```

## FEATURES

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source

```

## ORIGIN

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Alignment Scores:
Pred. No.: 2,96e-168 Length: 1218
Score: 1451.00 Matches: 272
Percent Similarity: 96.96% Conservative: 15
Best Local Similarity: 91.89% Mismatches: 9
Query Match: 94.04% Indels: 0
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US-09-811-094-33 (1-298) x CF110898 (1-1218)

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## QY

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 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
 DB 179 GGCAGCAAGCAATCAGCGCAGATAGCAATACAGGGCATCATAGTGGTGGTGGT 238  
 QY 61 IleProLysGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80  
 DB 239 ATCCCAAGACAGGAGTCTGCTCTCTGCGGTGGCACTGGCAATGTCTATCAGA 298  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
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 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
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 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
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 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180  
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 LOCUS AL540267 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
 DEFINITION CS0DF032YN01 5-PRIME, mRNA sequence.  
 ACCESSION AL540267  
 VERSION 1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 1201)  
 Li, W. B., Gruber, C., Jessee, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12870254.

Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 was not normalized. Library was constructed by Life Technologies, a  
 division of invitrogen. This sequence belongs to sequence cluster  
 10389.r For more information about this cluster, see  
 http://www.genoscope.cns.fr/  
 cgi-bin/cluster.cgi?seq=CS0DF032CG01QP1cluster=10389.r. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Paraday Avenue Genoscope sequence ID : CS0DF032CG01QP1.  
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 vector. Library was not normalized."

FEATURES  
source

## ORIGIN

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 Score: 1449.00 Matches: 286  
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 Best Local Similarity: 98.96% Mismatches: 3  
 Query Match: 93.91% Indels: 2  
 DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x AL540267 (1-1201)

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 DB 159 ATGACGGAACAGGCGCATCTCTTCGCCAAGACTTCTGGCCGAGGATC-GCCGCCGCC 217  
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40  
 DB 218 ATCTCCAAGACGGCGTGGCTCCGATCAGCGGGTCAAGCTGCTGCTGAGGTCCAGCAC 277  
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60  
 DB 278 GCCAGCAAGCAGATCGCGCGCACAGCAGTACAAAGGCGATCGTGGACTGCAATGTCGCC 337  
 QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80  
 DB 338 ATCCCAAGACGAGCGGGTGTCTCTCTTGGAGGGGCAACCTTGGCAAGCTCATTCGC 397  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
 DB 398 TACTTCCCACCTCAAGGCCCTCACTTCGCCCTTCAAGGATAAGTACAAAGCAGATCTTCTG 457  
 QY 101 GlyGlyValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120  
 DB 458 GGGGCGGTGGACAGCACACGACGTCCTTCTGGAGGTACTTTCGGGCAACCTTGGCCCTCCGGC 517  
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140  
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 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160  
 DB 578 CTGCAGCGGACGTGGGAAAGTCAAGCAGCAGCGGAGTTCGAGGGCTCGGAGACTGC 637  
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Pred. No.: 1.68e-167 Length: 1237  
 Score: 1445.00 Matches: 271  
 Percent Similarity: 96.62% Conservative: 15  
 Best Local Similarity: 91.55% Mismatches: 10  
 Query Match: 93.65% Indels: 0  
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US-09-811-094-33 (1-298) x AK012751 (1-1237)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyLeuAlaAala 20  
 DB 79 ATGACAGATGCCGCTGTGCTTCCCAAGAGCTTCTTGGCGGAGTGGCCGACCC 138  
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 QY 41 AlaSerLysGlnIleAlaAlaLysGlnTyrLysGlyIleValAspCysIleValArg 60  
 DB 199 GGCAGCAAGCAATACGCGCATAGCAATACAGGGCATCATAGCTGGTGGTTCGT 258  
 QY 61 IleProLysGlnGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80  
 DB 259 ATCCCAAGAACAGGGAGTCTGTCTTCTGGCGTGGGAACCTGGCCAAATGTCATCAGA 318  
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100  
 DB 319 TACTTCCCACCCAGGCTCTCACTTGTGCTTCAAGATAAATACAGCAGATCTTCTG 378  
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 DB 619 GTACAGGGCATTTATCATCTACCGAGCTGCTACTTGTGTATCTATGACATCTCAAGGGA 678  
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220  
 DB 679 ATGCTCCAGATCCCAAGATATCTCATCTTCATCAGCTGGATGATTCACAGCTGTC 738  
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240  
 DB 739 ACTGCTGCTGGCTGACTTCTTCTATCTTTGACACGGTTCGCGCTGATGATGATG 798  
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260  
 DB 799 CACTCTGGACGCAAGGAATGATATCATGTACACAGGCACGCTTGTACCTGGCGGAG 858  
 QY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280  
 DB 859 ATCCGCGCATAGAGGAGCAGGCTTTTTCAGGGCGCATGTGTCACAGCTTCTCAGA 918  
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296  
 DB 919 GGCATGGTGGCGCTTGTGCTTGTGCTTGTATGATGATGATCAAGAAA 966

RESULT 12

AK088730 1237 bp mRNA linear HTC 20-SBP-2003  
 LOCUS Mus musculus 2 days neonate thymic cells cDNA, RIKEN  
 DEFINITION

full-length enriched library, clone:E430024K03 product:solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, full insert sequence.

ACCESSION AK088730.1 GI:26353805  
 VERSION HTG; CAP trapper.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus

ORGANISM

REFERENCE  
 AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, O., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

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TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

full-length enriched library, clone:E430024K03 product:solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, full insert sequence.

ACCESSION AK088730.1 GI:26353805  
 VERSION HTG; CAP trapper.  
 KEYWORDS Mus musculus (house mouse)  
 SOURCE Mus musculus

REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.  
 TITLE High-efficiency full-length cDNA cloning  
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
 MEDLINE 99279253  
 PUBMED 10349636

REFERENCE

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
 MEDLINE 20499374  
 PUBMED 11042159

REFERENCE

AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, O., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861

REFERENCE

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation

JOURNAL Nature 420, 563-573 (2002)

REFERENCE

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohnato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

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REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

prepare mouse tissues.  
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.go.jp/>  
URL: <http://fantom.gsc.riken.go.jp/>.

## FEATURES

Source

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1. 1237
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CDS

polyA signal

polyA site

## ORIGIN

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Argument Scores:
Pred. No.:      1.60e-167      Length: 1237
Score:          145.00         Matches: 271
Percent Similarity: 96.63%      Conservative: 15
Best Local Similarity: 91.55%    Mismatches: 10
Query Match:      93.65%         Indels: 0
DB:               11            Gaps: 0

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US-09-811-094-33 (1-298) X AK088730 (1-1237)

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QY	21	IleSerLysThrAlaValAlaProIleuArgValLysLeuLeuLeuValGlnHis	40
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DB	198	GCCAGCAAGCAAAATCACGGCAGATAAGCAATACAAGGGCATCATGACTCGCTGTCTGT	257
QY	61	IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
DB	258	ATCCCCAAGGAACAGGGAGTCTCTGCTCTCTGCGGTGGGAACCTGGCCCAATGTCATCAGA	317
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QY	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
DB	378	GCTCGTGTGACAAGAGACCCAGTTCCTGCGCTACTTTTSCAGGAACTTCATCAGCT	437









http://image.llnl.gov  
 Plate: LAM14819 row: p column: 17  
 High quality sequence stop: 860.

## FEATURES

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 /lab\_host="DH10B"  
 /clone\_lib="NIH ZGC 10"  
 /note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;  
 Bulk tissue was collected from a whole adult individual  
 from the Tuebingen strain. 1st strand cDNA was primed with  
 a Not I - oligo(dT) primer, double-stranded cDNA was  
 cloned into the Not I and EcoRV sites of pExpress-1.  
 Library was size-selected for >1 kb fragments. A  
 normalized version of this library is also available  
 (NIH\_ZGC 7). Library was constructed by Open Biosystems  
 (Huntsville, AL)."

## ORIGIN

## Alignment Scores:

Pred. No.: 9,73e-167 Length: 1064  
 Score: 1438.00 Matches: 272  
 Percent Similarity: 96.64% Conservative: 16  
 Best Local Similarity: 91.28% Mismatches: 10  
 Query Match: 93.20% Indels: 0  
 DB: 14 Gaps: 0

US-09-811-094-33 (1-298) x CK024940 (1-1064)

Qy	1	MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyLeuAlaAla	20
Db	73	ATGAGTGAGCGCCATCTCTTCCCAAGGACTTCTTGGCGGTGGTATTGCGCGTGC	132
Qy	21	IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis	40
Db	133	ATCTCTAAACCGCGGTGGCCCATTCAGAGAGTCAACTGCTTCAGGTGCACAT	192
Qy	41	AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg	60
Db	193	GCTAGCAAAACAGATTACAGCAGATTAAGCAGTACAAAGGCAATTATGGACTGGTGGCGT	252
Qy	61	IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg	80
Db	253	ATCCCCAAGGACAGGGCTTCCTGTCTTGGAGAGGAACCTTGCCCAACGTATACGA	312
Qy	81	TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu	100
Db	313	TACTTCCCCACACAGGCCCTCAACTTTGCTTTCAAGGACAAGTACAAGAAGTCTTCCTT	372
Qy	101	GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly	120
Db	373	GATGTGTGGACAAGCGCACATCCCTCTGCTTGTGTATCCCTTGACTTCGCAAGAACCGGT	432
Qy	121	GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg	140
Db	433	GGTGTGTGTGGTGGCACATCCCTCTGCTTGTGTATCCCTTGACTTCGCAAGAACCGGT	492
Qy	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys	160
Db	493	CTTGTGTGGCGATGTGGAAAGCTGGAGCAGAAAGAGAGTTTCAGTGGGCTGGGTAACTGC	552
Qy	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer	180
Db	553	TTGGTAAAGATCTCCAAATCTTGATGCATCAAGGCTCTGTACAGGGCTTCAACGTGTCC	612
Qy	181	ValGlnGlyIleIleIleTyrArgAlaAlaLatyrPheGlyThrAspThrAlaLysGly	200
Db	613	GTGAGGGTATCATCATTTACAGAGCTGCTACTTCTGGCATTTATGACACAGCCCAAGGT	672

Search completed: August 17, 2004, 20:23:02

Job time : 2952 secs

Qy	201	MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal	220
Db	673	ATGCTCCCGATCCCAAGAACACCCCATATTGTGTGAGCTGGATGATTGCTCAGAGTGTG	732
Qy	221	ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet	240
Db	733	ACTGCTGTTGCTGCTCTTCTTCTTACCCCTTCGACACAGTGGTGGTGTATGATGATG	792
Qy	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
Db	793	CAGTCTGGACGTAAGGAGCTGACATCATGTACAGTGGCACAATTCAGTCTGGAGGAAG	852
Qy	261	IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg	280
Db	853	ATCGCACGTGATAGGCTGGCAAGGCTTCTTCAAGAGAGCCCTGGTCAACGTTCTCAGA	912
Qy	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLysValIle	298
Db	913	GGCATGGTGGCGCCCTTGTGCTGCTTGTGATGATGAGCTTGAGAAGGTCAATT	966

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